09/405,835

Search results for Page #10

Trying 3106016892...Open

Welcome to STN International! Enter x:x
LOGINID:ssspta1636txb
PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2	Sep 29	The Philippines Inventory of Chemicals and Chemical Substances (PICCS) has been added to CHEMLIST
NEWS 3	Oct 27	New Extraction Code PAX now available in Derwent Files
NEWS 4	Oct 27	SET ABBREVIATIONS and SET PLURALS extended in Derwent World Patents Index files
NEWS 5	Oct 27	Patent Assignee Code Dictionary now available in Derwent Patent Files
NEWS 6	Oct 27	Plasdoc Key Serials Dictionary and Echoing added to Derwent Subscriber Files WPIDS and WPIX
NEWS 7	Nov 29	Derwent announces further increase in updates for DWPI
NEWS 8	Dec 5	French Multi-Disciplinary Database PASCAL Now on STN
NEWS 9	Dec 5	Trademarks on STN - New DEMAS and EUMAS Files
NEWS 10	Dec 15	2001 STN Pricing
NEWS 11	Dec 17	Merged CEABA-VTB for chemical engineering and biotechnology
NEWS 12	Dec 17	Corrosion Abstracts on STN
NEWS 13	Dec 17	SYNTHLINE from Prous Science now available on STN
NEWS 14	Dec 17	The CA Lexicon available in the CAPLUS and CA files
NEWS 15	Jan 05	AIDSLINE is being removed from STN
NEWS EXPRESS		FREE UPGRADE 5.0e FOR STN EXPRESS 5.0 WITH DISCOVER! (WINDOWS) NOW AVAILABLE
NEWS HOURS		STN Operating Hours Plus Help Desk Availability
NEWS INTER		General Internet Information
NEWS LOGIN		Welcome Banner and News Items
NEWS PHONE		Direct Dial and Telecommunication Network Access to STN
NEWS WWW		CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

All use of STN is subject to the provisions of the STN Customer agreement. Please note that this agreement limits use to scientific research. Use for software development or design or implementation of commercial gateways or other similar uses is prohibited and may result in loss of user privileges and other penalties.

* * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001

=> file caplus, biosis, caba, ceaba

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.15	0.15

```
FILE 'CAPLUS' ENTERED AT 14:21:27 ON 21 JAN 2001
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2001 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'BIOSIS' ENTERED AT 14:21:27 ON 21 JAN 2001
COPYRIGHT (C) 2001 BIOSIS(R)

FILE 'CABA' ENTERED AT 14:21:27 ON 21 JAN 2001
COPYRIGHT (C) 2001 CAB INTERNATIONAL (CABI)

FILE 'CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001
COPYRIGHT (c) 2001 DECHEMA eV

=> s malate(W)synthase

L1         1274 MALATE(W) SYNTHASE

=> s promoter

L2       199155 PROMOTER

=> s germin

L3          203 GERMIN

=> glyoxysomal

GLYOXYSOMAL IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s glyoxysomal

L4          877 GLYOXYSOMAL

=> s aleutrone(W)layer

L5            0 ALEUTRONE(W) LAYER

=> s aleutrone

L6            0 ALEUTRONE

=> s carboxypeptidase

L7        13735 CARBOXYPEPTIDASE

=> glutathione(W)transferase

GLUTATHIONE(W)TRANSFERASE IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s glutathione(W)transferase

L8         8459 GLUTATHIONE(W) TRANSFERASE

=> s AlcA

L9          478 ALCA

=> s AlcR
```

```
L10         186 ALCR

=> s Iacc(P)repressor

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'IACC(P)REPRESSOR'
L11           0 IACC(P) REPRESSOR

=> s Iacc

L12          13 IACC

=> s 434

L13        6132 434

=> s p22

L14        4174 P22

=> s tet

L15        3352 TET

=> s repressor

L16       21064 REPRESSOR

=>  lambda(W)bacteriophage

LAMBDA(W)BACTERIOPHAGE IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s lambda(W)bacteriophage

L17         459 LAMBDA(W) BACTERIOPHAGE

=> d hist


     (FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

     FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001
L1          1274 S MALATE(W)SYNTHASE
L2        199155 S PROMOTER
L3           203 S GERMIN
L4           877 S GLYOXYSOMAL
L5             0 S ALEUTRONE(W)LAYER
L6             0 S ALEUTRONE
L7         13735 S CARBOXYPEPTIDASE
L8          8459 S GLUTATHIONE(W)TRANSFERASE
L9           478 S ALCA
L10          186 S ALCR
L11            0 S IACC(P)REPRESSOR
L12           13 S IACC
L13         6132 S 434
L14         4174 S P22
L15         3352 S TET
L16        21064 S REPRESSOR
L17          459 S LAMBDA(W)BACTERIOPHAGE

=> s l1(P)l2
```

```
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L4(P)L9'
L18          44 L1(P) L2

=> s l3(P)l2

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L14(P)L9'
L19          17 L3(P) L2

=> s l4(P)l2

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L19(P)L9'
L20          14 L4(P) L2

=> s l7(P)l2

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L34(P)L9'
L21         170 L7(P) L2

=> d hist


     (FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

     FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001
L1          1274 S MALATE(W)SYNTHASE
L2        199155 S PROMOTER
L3           203 S GERMIN
L4           877 S GLYOXYSOMAL
L5             0 S ALEUTRONE(W)LAYER
L6             0 S ALEUTRONE
L7         13735 S CARBOXYPEPTIDASE
L8          8459 S GLUTATHIONE(W)TRANSFERASE
L9           478 S ALCA
L10          186 S ALCR
L11            0 S IACC(P)REPRESSOR
L12           13 S IACC
L13         6132 S 434
L14         4174 S P22
L15         3352 S TET
L16        21064 S REPRESSOR
L17          459 S LAMBDA(W)BACTERIOPHAGE
L18           44 S L1(P)L2
L19           17 S L3(P)L2
L20           14 S L4(P)L2
L21          170 S L7(P)L2

=> s l8(P)l2

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L39(P)L9'
L22          72 L8(P) L2

=> s l9(P)l2

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L44(P)L9'
L23          84 L9(P) L2

=> s l10(P)l2
```

```
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L49(P)L9'
L24          36 L10(P) L2

=> s l12(P)12

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L59(P)L9'
L25           0 L12(P) L2

=> d hist


     (FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

     FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001
L1          1274 S MALATE(W)SYNTHASE
L2        199155 S PROMOTER
L3           203 S GERMIN
L4           877 S GLYOXYSOMAL
L5             0 S ALEUTRONE(W)LAYER
L6             0 S ALEUTRONE
L7         13735 S CARBOXYPEPTIDASE
L8          8459 S GLUTATHIONE(W)TRANSFERASE
L9           478 S ALCA
L10          186 S ALCR
L11            0 S IACC(P)REPRESSOR
L12           13 S IACC
L13         6132 S 434
L14         4174 S P22
L15         3352 S TET
L16        21064 S REPRESSOR
L17          459 S LAMBDA(W)BACTERIOPHAGE
L18           44 S L1(P)L2
L19           17 S L3(P)L2
L20           14 S L4(P)L2
L21          170 S L7(P)L2
L22           72 S L8(P)L2
L23           84 S L9(P)L2
L24           36 S L10(P)L2
L25            0 S L12(P)L2

=> s l13(P)l16

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L64(P)L79'
L26         356 L13(P) L16

=> s l14(P)l16

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L69(P)L79'
L27         289 L14(P) L16

=> s l15(P)l16

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L74(P)L79'
L28         419 L15(P) L16

=> s l17(P)l16

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L84(P)L79'
L29          12 L17(P) L16
```

```
=> d his

     (FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

     FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001
L1          1274 S MALATE(W)SYNTHASE
L2        199155 S PROMOTER
L3           203 S GERMIN
L4           877 S GLYOXYSOMAL
L5             0 S ALEUTRONE(W)LAYER
L6             0 S ALEUTRONE
L7         13735 S CARBOXYPEPTIDASE
L8          8459 S GLUTATHIONE(W)TRANSFERASE
L9           478 S ALCA
L10          186 S ALCR
L11            0 S IACC(P)REPRESSOR
L12           13 S IACC
L13         6132 S 434
L14         4174 S P22
L15         3352 S TET
L16        21064 S REPRESSOR
L17          459 S LAMBDA(W)BACTERIOPHAGE
L18           44 S L1(P)L2
L19           17 S L3(P)L2
L20           14 S L4(P)L2
L21          170 S L7(P)L2
L22           72 S L8(P)L2
L23           84 S L9(P)L2
L24           36 S L10(P)L2
L25            0 S L12(P)L2
L26          356 S L13(P)L16
L27          289 S L14(P)L16
L28          419 S L15(P)L16
L29           12 S L17(P)L16

=> d l18 1-10abs so,ti,abs,au

'1-10ABS' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files.  Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):

REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):

REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):ti


L18  ANSWER 1 OF 44  CAPLUS  COPYRIGHT 2001 ACS
TI   Cross-induction of glc and ace operons of Escherichia coli attributable
to
     pathway intersection. Characterization of the glc promoter


=> d his


     (FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

     FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001
L1          1274 S MALATE(W)SYNTHASE
L2        199155 S PROMOTER
```

```
L3          203 S GE[redacted]N
L4          877 S GL[redacted]YSOMAL
L5            0 S ALEUTRONE(W)LAYER
L6            0 S ALEUTRONE
L7        13735 S CARBOXYPEPTIDASE
L8         8459 S GLUTATHIONE(W)TRANSFERASE
L9          478 S ALCA
L10         186 S ALCR
L11           0 S IACC(P)REPRESSOR
L12          13 S IACC
L13        6132 S 434
L14        4174 S P22
L15        3352 S TET
L16       21064 S REPRESSOR
L17         459 S LAMBDA(W)BACTERIOPHAGE
L18          44 S L1(P)L2
L19          17 S L3(P)L2
L20          14 S L4(P)L2
L21         170 S L7(P)L2
L22          72 S L8(P)L2
L23          84 S L9(P)L2
L24          36 S L10(P)L2
L25           0 S L12(P)L2
L26         356 S L13(P)L16
L27         289 S L14(P)L16
L28         419 S L15(P)L16
L29          12 S L17(P)L16

=> d l18 1-10 abs,so,ti


L18  ANSWER 1 OF 44  CAPLUS  COPYRIGHT 2001 ACS
AB   The metabolic pathways specified by the glc and ace operons in
Escherichia
     coli yield glyoxylate as a common intermediate, which is acted on by two
     malate synthase isoenzymes: one encoded by glcB and the
     other by aceB.  Null mutations in either gene exhibit no phenotype,
     because of cross-induction of the ace operon by glycolate and the glc
     operon by acetate.  In this study, the regulation of the glc operon,
     comprising the structural genes glcDEFGB, was analyzed at the mol. level.
     This operon, activated by growth on glycolate, is transcribed as a single
     message and is under the pos. control of GlcC encoded by a divergent
gene.
     Expression of the glc operon is strongly dependent on the integration
host
     factor (IHF) and is repressed by the global respiratory regulator ArcA-P.
     In vitro gel-shift expts. demonstrated direct binding of the
     promoter DNA to IHF and ArcA-P.  Mutant anal. indicated that
     cross-induction of the glc operon by acetate is mediated by the GlcC
     protein that recognizes the compd. as an alternative effector.  The
     similar pattern of regulation of the Glc and Ace systems by IHF and
ArcA-P
     ensures their effective cross-induction.
SO   J. Biol. Chem. (1999), 274(3), 1745-1752
     CODEN: JBCHA3; ISSN: 0021-9258
TI   Cross-induction of glc and ace operons of Escherichia coli attributable
to
     pathway intersection. Characterization of the glc promoter

L18  ANSWER 2 OF 44  CAPLUS  COPYRIGHT 2001 ACS
AB   Malate synthase is a key enzyme of the glyoxylate
     cycle, which is an anaplerotic pathway essential for growth on acetate as
     the sole carbon source.  The aceB gene, encoding malate
     synthase from Streptomyces clavuligerus NRRL 3585, was cloned
     using PCR and fully sequenced.  The ORF obtained encodes 541 amino acids
```

with a deduced M of 60,000, consistent with the reported Mr (62,000-64,000) of most **malate synthase** enzymes reported so far. The aceB gene has a high G+C content (71.5 mol%), esp. in the third codon position. A 50 bp region upstream of the **malate synthase** ORF was predicted to be a prokaryotic **promoter** region. The relationship between carbon source, antibiotic (cephalosporin) biosynthesis and **malate synthase** activity was investigated. Growth of S. clavuligerus on acetate as the major carbon source was delayed, compared to that on glycerol. Furthermore, high levels of **malate synthase** activity were assocd. with the presence of acetate in the growth medium. Growth on acetate also resulted in lower levels of cephalosporin prodn., compared to that on glycerol. The cloned S. clavuligerus aceB gene was expressed in Escherichia coli BL21(DE3). Transformants exhibited an approx. 71-fold increase in **malate synthase** activity, compared to the control, thereby demonstrating high-level expression of sol. and enzymically active **malate synthase** in the heterologous host.

SO Microbiology (Reading, U. K.) (1998), 144(11), 3229-3237
CODEN: MROBEO; ISSN: 1350-0872

TI Malate synthase from Streptomyces clavuligerus NRRL 3585: cloning, molecular characterization and its control by acetate

L18 ANSWER 3 OF 44 CAPLUS COPYRIGHT 2001 ACS

AB A method is provided for the selective control of seed germination, wherein germination can be inhibited by expression of a germination inhibitor and, subsequently, germination can be induced via an inducible promoter that is operably linked to a germination restorer. An example of the germination inhibitor is the antisense RNA specific to the soybean acyl CoA oxidase mRNA, and over-expression of the yeast acyl CoA oxidase gene was an example of the germination restorer. The acyl CoA oxidase was necessary for plant lipid mobilization. The Candida tropicalis acyl CoA oxidase genes POX4 and POX5 were expressed via plasmid vectors in transgenic Arabidopsis. Also disclosed are plants, plant cells, seeds and DNA constructs that are genetically engineered for control of seed germination.

SO PCT Int. Appl., 90 pp.
CODEN: PIXXD2

TI Method for controlling seed germination using soybean acyl CoA oxidase gene sequences

L18 ANSWER 4 OF 44 CAPLUS COPYRIGHT 2001 ACS

AB This invention relates to compns. and methods useful in the prodn. of transgenic plants. In particular, the invention relates to developmentally regulated **malate synthase** and isocitrate lyase Brassica napus **promoter** sequences (.ltoreq.3000 nucleotides) which are useful for directing expression of heterologous DNA sequences in seeds and seedlings. The invention also relates to expression cassettes contg. the **promoter** sequences and to transgenic plants such as Brassica and Arabidopsis contg. the expression cassettes. The invention can also be applied in com. valuable plant, including both dicots and monocots.

SO U.S., 28 pp.
CODEN: USXXAM

TI Brassica napus **malate synthase** and isocitrate lyase gene **promoter** sequences useful for gene expression in seeds and seedlings

L18 ANSWER 5 OF 44 CAPLUS COPYRIGHT 2001 ACS

AB The **malate synth[redacted]e** gene, MLS1, of the yeast Saccharomyces c[redacted]visiae is transcriptionally re[redacted]ated by the carbon source in the growth medium. A MLS1-lacZ fusion gene, expressed at a basal level in the presence of 2% glucose, is derepressed more than 100-fold under conditions of sugar limitation. No evidence for MLS1 induction by oleic acid was found. By deletion anal. of the MLS1 control region, two sites, UAS1 and UAS2, were identified as important for efficient derepression of the gene. Both sites contain sequences that resemble the previously characterized carbon source-responsive element (CSRE) found in the **promoter** of the isocitrate lyase gene ICL1. Indeed, UAS1 and UAS2 in the MLS1 upstream region turn out to be functional CSRE sequence variants. This finding allowed us to define a modified version of the CSRE consensus sequence (CCRTYSRNCCG). Protein binding to UAS1MLS1 was obsd. with exts. from derepressed but not from repressed cells, and could be competed for by an excess of the unlabeled CSRE(ICL1) sequence. No competition was obsd. with a mutated CSRE variant. Site-directed mutagenesis of both CSREs in the MLS1 **promoter** reduced gene activation under derepressing conditions to 20% of the wild-type level. The same decrease was obsd. with the wild-type MLS1 **promoter** in a cat8 mutant, lacking an activator of CSRE-dependent transcription. The CSRE/Cat8p-independent activation of MLS1 is mediated by constitutive UAS elements. The pleiotropic transcription factor Abf1p, which binds to the MLS1 upstream region, may contribute to constitutive activation. Thus, to ensure the severe glucose repression of MLS1 obsd., repressor elements that respond to the carbon source must counteract constitutive activation. In summary, ICL1 and MLS1 share common cis-acting elements, although a distinct mechanism of carbon source control also contributes to MLS1 regulation.

SO Mol. Gen. Genet. (1997), 255(6), 619-627
CODEN: MGGEAE; ISSN: 0026-8925

TI Constitutive and carbon source-responsive **promoter** elements are involved in the regulated expression of the Saccharomyces cerevisiae **malate synthase** gene MLS1

L18 ANSWER 6 OF 44 CAPLUS COPYRIGHT 2001 ACS

AB Recent data have shown that distinct DNA sequence elements direct the germination and sugar responses of the cucumber (Cucumis sativus) **malate synthase** (Ms) gene. Such information is, however, lacking for the isocitrate lyase (Icl) gene which is coordinately regulated with Ms. Deletions from the 5' end of the Icl **promoter** were therefore created specifically to address this question. Anal. of expression in seeds of transgenic Nicotiana plumbaginifolia plants showed that whereas a **promoter** sequence of 2.9 kb produced a normal germination response, deletion to -1568 bp dramatically reduced this response. Examn. of the sugar response employed a transgenic cucumber root system. In this case, the 2900-bp and 1568-bp promoters both gave a strong sugar response, but further deletion to -1367-bp eliminated the response. Therefore, the germination and sugar responses of the Icl gene require distinct cis-acting elements, located resp. upstream and downstream of -1568 bp. This observation is consistent with distinct signal transduction systems regulating gene expression in each case.

SO Gene (1997), 197(1/2), 375-378
CODEN: GENED6; ISSN: 0378-1119

TI Distinct cis-acting sequences are required for the germination and sugar responses of the cucumber isocitrate lyase gene

L18 ANSWER 7 OF 44 CAPLUS COPYRIGHT 2001 ACS

AB The glyoxylate cycle, catalyzed by two unique enzymes: isocitrate lyase (ICL; EC 4.1.3.1) and **malate synthase** (MS; EC 4.1.3.2), is necessary for the net conversion of acetate into glucose. This metabolic pathway operates in microorganisms, higher plants and

nematodes. Two bacterial genes, encoding ICL and MS, were modified in order to introduce them into the mouse germ line. The ovine metallothionein-Ia (MT-Ia) **promoter**-ace B gene-ovine growth hormone (GH) gene (3' GH sequence) construct was fused to the ovine MT-Ia **promoter**-ace A gene-ovine GH gene (3' GH seguence). Therefore, in this single DNA sequence, both aceA and aceB are under independent MT-Ia **promoter** control and can be induced by zinc. Transgenic mice were generated by pronuclear microinjection of the aceB-aceA gene construct. We no report the establishment of four mouse lines carrying these two transgenes. Studies on the progeny of these lines indicate that one line (No. 91) is expressing both genes at the mRNA and enzyme levels in the liver and intestine, whereas another line (No. 66) has a much lower expression. Both enzyme activities were detected in the liver and intestine at levels up to 25% of those measured in fully derepressed Escherichia coli cells.

SO Transgenic Res. (1996), 5(6), 467-473
CODEN: TRSEES; ISSN: 0962-8819

TI Introduction and expression of the bacterial glyoxylate cycle genes in transgenic mice

L18 ANSWER 8 OF 44 CAPLUS COPYRIGHT 2001 ACS

AB The **malate synthase** gene (ms) **promoter** in cucumber (Cucumis sativus L.) was investigated with the aim of distinguishing DNA sequences mediating regulation of gene expression by sugar, and expression following seed germination. **Promoter** deletions were constructed and their ability to direct expression of the .beta.-glucuronidase (gus) reporter gene was investigated in transgenic Nicotiana plumbaginifolia. Gene expression was assayed in germinating seeds and developing seedlings (the germination response) and in seedlings transferred from light into darkness with and without sucrose (the sugar response). As progressively more of the **promoter** was deleted from the 5' end, first the sugar response and then the germination response was lost. Thus, distinct regions of the **promoter** are required for carbohydrate control and for regulation of gene expression in response to germination. Sequence comparisons of the ms **promoter** with that of the isocitrate lyase gene (icl) of cucumber have previously identified four IMH (ICL-MS Homol.) sequences. One such sequence, IMH2, is shown here to be implicated in the sugar response of the ms gene. The 17 bp sequence, which when deleted from the ms gene results in loss of the germination response, contains a 14 bp seguence which is similar to a sequence in the icl **promoter**, which the authors refer to as IMH5. Furthermore, this sequence has similarity with amdI9-like sequences in filamentous fungi, which confer facB-mediated acetate inducibility on several genes, including those encoding ICL and MS.

SO Mol. Gen. Genet. (1996), 250(2), 153-61
CODEN: MGGEAE; ISSN: 0026-8925

TI Distinct cis-acting elements direct the germination and sugar responses of the cucumber malate synthase gene

L18 ANSWER 9 OF 44 CAPLUS COPYRIGHT 2001 ACS

AB Expression of the genes encoding several peroxisomal enzymes of the n-alkane-utilizable yeast Candida tropicalis has been examd. in Saccharomyces cerevisiae to find out a novel and foreign **promoter** functional in S. cerevisiae. Among these genes, two **malate synthase** genes, as well as the isocitrate lyase gene, were strongly expressed in acetate-grown cells of S. cerevisiae. The amts. of the recombinant malate synthases expressed in S. cerevisiae were as much as 30% of the total amt. of sol. proteins in the cells. These results showed that the upstream regions (1.1 kbp for the MS-1 gene and 0.8 kbp for the MS-2 gene) of the **malate synthase** genes

[UPR-MSs] from C. tropicalis contained strong **promoter** functional in S. cerevisiae and that the construction of novel gene expression systems using UPR-MSs might be possible.

SO J. Ferment. Bioeng. (1996), 81(1), 61-3
CODEN: JFBIEX; ISSN: 0922-338X

TI Strong expression of peroxisomal malate synthase genes from n-alkane-utilizable yeast Candida tropicalis in Saccharomyces cerevisiae

L18 ANSWER 10 OF 44 CAPLUS COPYRIGHT 2001 ACS

AB A regulatable **promoter** derived from the **malate synthase** gene of Corynebacterium is claimed. Expression vectors contg. this **promoter**, recombinant Corynebacterium contg. these vectors, and a method for prepg. proteins using these bacteria are addnl. claimed. An expression vector contg. the chlormaphenicol acetyltransferase gene fused to the aceB gene **promoter** was introduced into C. glutamicum. The expression of this reporter gene was regulated by the C source in the medium. Acetate stimulated synthesis of the enzyme better than pyruvate or lactate.

SO Ger., 12 pp.
CODEN: GWXXAW

TI Corynebacterium **malate synthase** gene **promoter** and its use in regulatable expression of genes in recombinant Corynebacterium

=> d l18 10 ibib

L18 ANSWER 10 OF 44 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1995:997034 CAPLUS
DOCUMENT NUMBER: 124:78713
TITLE: Corynebacterium **malate synthase** gene **promoter** and its use in regulatable expression of genes in recombinant Corynebacterium
INVENTOR(S): Reinscheid, Dieter; Eikmanns, Berndhard; Sahm, Hermann
PATENT ASSIGNEE(S): Forschungszentrum Juelich GmbH, Germany
SOURCE: Ger., 12 pp.
CODEN: GWXXAW
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 4440118	C1	19951109	DE 1994-4440118	19941111
WO 9615246	A1	19960523	WO 1995-DE1555	19951107
W: CN, JP, KR, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 791062	A1	19970827	EP 1995-936429	19951107
R: DE, FR, GB, IE, IT, NL, SE				
CN 1174574	A	19980225	CN 1995-197304	19951107
JP 10512742	T2	19981208	JP 1995-515635	19951107
ZA 9509598	A	19960528	ZA 1995-9598	19951113
US 5965391	A	19991012	US 1997-836943	19970508
PRIORITY APPLN. INFO.:			DE 1994-4440118	19941111
			WO 1995-DE1555	19951107

=> d l18 1-10 ibib

L18 ANSWER 1 OF 44 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:95748 CAPLUS

DOCUMENT NUMBER: 130:277570
TITLE: Cross-induction of glc and ac[redacted]operons of Escherichia coli attributable to pathway intersection. Characterization of the glc promoter
AUTHOR(S): Pellicer, Maria Teresa; Fernandez, Carmen; Badia, Josefa; Aguilar, Juan; Lin, Edmund C. C.; Baldoma, Laura
CORPORATE SOURCE: Department of Biochemistry, School of Pharmacy, University of Barcelona, Barcelona, 08028, Spain
SOURCE: J. Biol. Chem. (1999), 274(3), 1745-1752
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 43
REFERENCE(S): (2) Baldoma, L; J Biol Chem 1987, V262, P13991 CAPLUS
(3) Belasco, J; Cell 1985, V40, P171 CAPLUS
(4) Boronat, A; J Bacteriol 1979, V140, P320 CAPLUS
(5) Boronat, A; J Bacteriol 1981, V147, P181 CAPLUS
(7) Chung, T; J Bacteriol 1988, V170, P386 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 2 OF 44 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:753592 CAPLUS
DOCUMENT NUMBER: 130:135702
TITLE: Malate synthase from Streptomyces clavuligerus NRRL 3585: cloning, molecular characterization and its control by acetate
AUTHOR(S): Chan, Maurice; Sim, Tiow-Suan
CORPORATE SOURCE: Department of Microbiology, National University of Singapore, Singapore, 119260, Singapore
SOURCE: Microbiology (Reading, U. K.) (1998), 144(11), 3229-3237
CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 31
REFERENCE(S): (1) Aharonowitz, Y; Antimicrob Agents Chemother 1978, V14, P159 CAPLUS
(2) Alves, A; J Bacteriol 1994, V176, P6827 CAPLUS
(3) Bibb, M; Gene 1984, V30, P157 CAPLUS
(4) Brana, A; Can J Microbiol 1985, V31, P736 CAPLUS
(5) Brendel, V; J Mol Evol 1997, V44, P528 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 3 OF 44 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:776268 CAPLUS
DOCUMENT NUMBER: 128:58322
TITLE: Method for controlling seed germination using soybean acyl CoA oxidase gene sequences
INVENTOR(S): Agarwal, Ametta Kishore; Brown, Sherri Marie; Qi, Youlin
PATENT ASSIGNEE(S): Monsanto Company, USA
SOURCE: PCT Int. Appl., 90 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9744465	A1	19971127	WO 1997-US8732	19970520

W: AL, AM, [redacted] AU, AZ, BA, BB, BG, BR, BY, [redacted] CH, CN, CU, CZ, DE, DK, EE, [redacted] FI, GB, GE, GH, HU, IL, IS, [redacted] KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

AU 9731394	A1	19971209	AU 1997-31394 19970520
PRIORITY APPLN. INFO.:			US 1996-17614 19960520
			WO 1997-US8732 19970520

L18 ANSWER 4 OF 44 CAPLUS ~~COPYRIGHT~~ 2001 ACS
ACCESSION NUMBER: 1997:752802 CAPLUS
DOCUMENT NUMBER: 128:58290
TITLE: Brassica napus **malate synthase** and isocitrate lyase gene **promoter** sequences useful for gene expression in seeds and seedlings
INVENTOR(S): Harada, John J.; Zhang, James Z.; Laudencia-Chingcuanco, Debbie
PATENT ASSIGNEE(S): Regents of the University of California, USA
SOURCE: U.S., 28 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5689040	A	19971118	US 1995-393219	19950223

L18 ANSWER 5 OF 44 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:639321 CAPLUS
DOCUMENT NUMBER: 127:315521
TITLE: Constitutive and carbon source-responsive **promoter** elements are involved in the regulated expression of the Saccharomyces cerevisiae **malate synthase** gene MLS1
AUTHOR(S): Caspary, F.; Hartig, A.; Schuller, H.-J.
CORPORATE SOURCE: Biochem. Genetik, Lehrstuhl Biochem., Inst. Mikrobiol., Erlangen, D-91058, Germany
SOURCE: Mol. Gen. Genet. (1997), 255(6), 619-627
CODEN: MGGEAE; ISSN: 0026-8925
PUBLISHER: Springer
DOCUMENT TYPE: Journal
LANGUAGE: English

L18 ANSWER 6 OF 44 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:555535 CAPLUS
DOCUMENT NUMBER: 127:258505
TITLE: Distinct cis-acting sequences are required for the germination and sugar responses of the cucumber isocitrate lyase gene
AUTHOR(S): De Bellis, Luigi; Ismail, Ismanizan; Reynolds, Susan J.; Barrett, Matthieu D.; Smith, Steven M.
CORPORATE SOURCE: Institute of Cell and Molecular Biology, University of Edinburgh, The King's Buildings, Mayfield Road, Edinburgh, EH9 3JH, UK
SOURCE: Gene (1997), 197(1/2), 375-378
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

L18 ANSWER 7 OF 44 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:623735 CAPLUS
DOCUMENT NUMBER: 125:266882
TITLE: Introduction and expression of the bacterial glyoxylate cycle genes in transgenic mice
AUTHOR(S): Saini, Kulvinder S.; Byrne, Carolyn R.; Leish, Zdenka; Pruss, Cathy A.; Rigby, Nola W.; Brownlee, Alan G.; Nancarrow, Colin D.; Ward, Kevin A.
CORPORATE SOURCE: CSIRO, Div. of Animal Prodn., Prospect, NSW 2149, Australia
SOURCE: Transgenic Res. (1996), 5(6), 467-473
CODEN: TRSEES; ISSN: 0962-8819
DOCUMENT TYPE: Journal
LANGUAGE: English

L18 ANSWER 8 OF 44 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:157763 CAPLUS
DOCUMENT NUMBER: 124:222616
TITLE: Distinct cis-acting elements direct the germination and sugar responses of the cucumber malate synthase gene
AUTHOR(S): Sarah, Caroline J.; Graham, Ian A.; Reynolds, Susan J.; Leaver, Christopher J.; Smith, Steven M.
CORPORATE SOURCE: Inst. Cell, Univ. Edinburgh, Edinburgh, EH9 3JH, UK
SOURCE: Mol. Gen. Genet. (1996), 250(2), 153-61
CODEN: MGGEAE; ISSN: 0026-8925
DOCUMENT TYPE: Journal
LANGUAGE: English

L18 ANSWER 9 OF 44 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:99099 CAPLUS
DOCUMENT NUMBER: 124:166698
TITLE: Strong expression of peroxisomal malate synthase genes from n-alkane-utilizable yeast Candida tropicalis in Saccharomyces cerevisiae
AUTHOR(S): Murai,; Toshiyuki; Atomi, Hariyuki; Ueda, Mitsuyoshi; Tanaka, Atsuo
CORPORATE SOURCE: Lab. Appl. Biol. Chem., Kyoto Univ., Kyoto, 606-01, Japan
SOURCE: J. Ferment. Bioeng. (1996), 81(1), 61-3
CODEN: JFBIEX; ISSN: 0922-338X
DOCUMENT TYPE: Journal
LANGUAGE: English

L18 ANSWER 10 OF 44 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:997034 CAPLUS
DOCUMENT NUMBER: 124:78713
TITLE: Corynebacterium **malate synthase** gene **promoter** and its use in regulatable expression of genes in recombinant Corynebacterium
INVENTOR(S): Reinscheid, Dieter; Eikmanns, Berndhard; Sahm, Hermann
PATENT ASSIGNEE(S): Forschungszentrum Juelich GmbH, Germany
SOURCE: Ger., 12 pp.
CODEN: GWXXAW
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

DE 4440118	C1	19951109	DE 1994-4440118	19941111
WO 9615246	A1	19960523	WO 1995-DE1555	19951107
W: CN, JP, KR, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 791062	A1	19970827	EP 1995-936429	19951107
R: DE, FR, GB, IE, IT, NL, SE				
CN 1174574	A	19980225	CN 1995-197304	19951107
JP 10512742	T2	19981208	JP 1995-515635	19951107
ZA 9509598	A	19960528	ZA 1995-9598	19951113
US 5965391	A	19991012	US 1997-836943	19970508
PRIORITY APPLN. INFO.:			DE 1994-4440118	19941111
			WO 1995-DE1555	19951107

=> d his

(FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001

L1	1274	S	MALATE(W)SYNTHASE
L2	199155	S	PROMOTER
L3	203	S	GERMIN
L4	877	S	GLYOXYSOMAL
L5	0	S	ALEUTRONE(W)LAYER
L6	0	S	ALEUTRONE
L7	13735	S	CARBOXYPEPTIDASE
L8	8459	S	GLUTATHIONE(W)TRANSFERASE
L9	478	S	ALCA
L10	186	S	ALCR
L11	0	S	IACC(P)REPRESSOR
L12	13	S	IACC
L13	6132	S	434
L14	4174	S	P22
L15	3352	S	TET
L16	21064	S	REPRESSOR
L17	459	S	LAMBDA(W)BACTERIOPHAGE
L18	44	S	L1(P)L2
L19	17	S	L3(P)L2
L20	14	S	L4(P)L2
L21	170	S	L7(P)L2
L22	72	S	L8(P)L2
L23	84	S	L9(P)L2
L24	36	S	L10(P)L2
L25	0	S	L12(P)L2
L26	356	S	L13(P)L16
L27	289	S	L14(P)L16
L28	419	S	L15(P)L16
L29	12	S	L17(P)L16

=> d l19 1-10 abs ibib

L19 ANSWER 1 OF 17 CAPLUS COPYRIGHT 2001 ACS

AB The present project aimed to isolate testa-, pericarp- and epicarp-specific gene promoters for the developing caryopsis of barley (Hordeum vulgare L.). These might be applied in transgenic plants to express antifungal agents or modify metabolic pathways. A testa-specific 379-nucleotide fragment was cloned by differential amplification and used to screen a bacterial artificial chromosome (BAC) library of 6.3 haploid genome equiv. Fifty-three clones contg. genes encoding for proteins of the **germin** family were found. Characterization of the clones identified a min. of six seed coat- and eight leaf-specific **germin** genes. Four seed coat- and one leaf-specific genes were sequenced. The deduced primary structure of the proteins revealed a remarkable

conservation of [redacted]e manganese(II) binding His and [redacted]lu residues and .beta.-barrel s[redacted]dary structure of oxalate oxid[redacted] - also in barley, wheat, rice and Arabidopsis germins, for which an enzymic activity has not yet been identified. The oxalate oxidase and germins of barley and other species are synthesized with a conserved pre-sequence of 23 or 24 amino acids for targeting into the cell wall. .beta.-Glucuronidase expression with the barley **germin** F gene **promoter** occurs specifically in the testa and epicarp of the developing barley caryopsis, while expression with the B gene **promoter** is restricted to the testa. Oxalate oxidase activity is prominent in the epicarp and the root tips of the developing embryo. A family tree based on primary structure homologies of germins distinguishes three groups: oxalate oxidases, leaf-specific germins and seed coat-specific germins.

ACCESSION NUMBER: 2000:799118 CAPLUS
TITLE: Functional characterization of seed coat-specific members of the barley germin gene family
AUTHOR(S): Wu, Shiping; Druka, Arnis; Horvath, Henriette; Kleinhofs, Andris; Kannangara, C. Gamini; Von Wettstein, Diter
CORPORATE SOURCE: Departments of Crop and Soil Sciences & Genetics and Cell Biology, Washington State University, Pullman, WA, 99164, USA
SOURCE: Plant Physiol. Biochem. (Paris) (2000), 38(9), 685-698
CODEN: PPBIEX; ISSN: 0981-9428
PUBLISHER: Editions Scientifiques et Medicales Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 32
REFERENCE(S):
(1) Berna, A; Plant Mol Biol 1997, V33, P417 CAPLUS
(2) Berna, A; Plant Mol Biol 1999, V39, P539 CAPLUS
(3) Caliskan, M; Plant J 1998, V15, P165 CAPLUS
(4) Dumas, B; Plant Physiol 1995, V107, P1091 CAPLUS
(5) Dunwell, J; Biotech Genet Eng Rev 1998, V15, P1 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L19 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2001 ACS
AB In Arabidopsis thaliana, steady-state abundance of the Atger3 transcript encoding a **germin**-like cell wall protein follows a circadian rhythm, reaching its highest level at the beginning of the night. As a first step towards dissecting the mol. mechanisms underlying these transcript oscillations, the Atger3 genomic locus was characterized. Transcriptional fusions of 1.8 kb and 967 bp Atger3 **promoter** fragments to the .beta.-glucuronidase (GUS) reporter gene mediate high-amplitude circadian oscillations of the GUS transcript in transgenic Arabidopsis. 5' Deletion to -490 greatly reduces overall transcript abundance while retaining a basal oscillation. Further deletion to -299 abolishes preferential GUS expression in the evening. Taken together, these data indicate that clock-response elements contributing to high-amplitude Atger3 oscillations largely reside between -299 and -967. Histochem. staining for GUS activity indicates that the Atger3 **promoter** is active in cotyledons, young leaves, petioles, the inflorescence axis, pedicels, sepals, ovary, style and siliques but not in roots, petals and anthers.

ACCESSION NUMBER: 1999:613790 CAPLUS
DOCUMENT NUMBER: 131:347399
TITLE: The Atger3 promoter confers circadian clock-regulated transcription with peak expression at the beginning of the night
AUTHOR(S): Staiger, Dorothee; Apel, Klaus; Trepp, Gian
CORPORATE SOURCE: Institute for Plant Sciences, ETH Center, Swiss

SOURCE: Federal Institute of Technolo[redacted] Zurich, 8092, Switz.
Plant Mol. Biol. (1999), 40(5[redacted] 873-882
CODEN: PMBIDB; ISSN: 0167-4412
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 57
REFERENCE(S): (2) Beator, J; Chronobiol Int 1996, V13, P319 CAPLUS
(3) Bechtold, N; CR Acad Sci Paris Sci Vie/Life Sci 1993, V316, P1194 CAPLUS
(4) Berna, A; Plant Mol Biol 1999, V39, P539 CAPLUS
(5) Bevan, M; Nucl Acids Res 1984, V12, P8711 CAPLUS
(8) Burke, T; Mol Gen Genet 1988, V213, P435 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L19 ANSWER 3 OF 17 CAPLUS COPYRIGHT 2001 ACS
AB Germins and **germin**-like proteins (GLPs) constitute a ubiquitous family of plant proteins that seem to be involved in many developmental and stress-related processes. Wheat **germin** has been extensively studied at the biochem. level: it is found in the apoplast and the cytoplasm of germinating embryo cells and it has oxalate oxidase activity (EC 1.2.3.4). **Germin** synthesis can also be induced in adult wheat leaves by auxins and by a fungal pathogen but it remains to be detd. whether the same gene is involved in developmental, hormonal, and stress response. In this work, the authors have studied the expression of one of the wheat **germin** genes, named gf-2.8, in wheat as well as in transgenic tobacco plants transformed with either this intact gene or constructs with GUS driven by its **promoter**. This has allowed us to demonstrate that expression of this single gene is both developmentally and pathogen-regulated. In addn., the authors show that expression of the wheat gf-2.8 **germin** gene is also stimulated by some abiotic stresses, esp. the heavy metal ions Cd2+, Cu2+, and Co2+. Several chems. involved in stress signal transduction pathways were also tested: only polyamines were shown to stimulate expression of this gene. Because regulation of the wheat gf-2.8 **germin** gene is complex and because its product results in developmental and stress-related release of hydrogen peroxide in the apoplast, it is likely that it plays an important role in several aspects of plant growth and defense mechanisms.
ACCESSION NUMBER: 1999:214686 CAPLUS
DOCUMENT NUMBER: 131:1562
TITLE: Regulation by biotic and abiotic stress of a wheat germin gene encoding oxalate oxidase, a H2O2-producing enzyme
AUTHOR(S): Berna, Anne; Bernier, Francois
CORPORATE SOURCE: Institut de Biologie Moleculaire des Plantes, Institut de Botanique, Strasbourg, 67083, Fr.
SOURCE: Plant Mol. Biol. (1999), 39(3), 539-549
CODEN: PMBIDB; ISSN: 0167-4412
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 43
REFERENCE(S): (1) Angelini, R; J Plant Physiol 1993, V142, P704 CAPLUS
(3) Berna, A; Phytopathology 1995, V85, P1441 CAPLUS
(4) Berna, A; Plant Mol Biol 1997, V33, P417 CAPLUS
(5) Bernier, F; Gene 1987, V59, P265 CAPLUS

(6) Braun, H; Plant Mol Biol [illegible]6, V31, P35 CAPLUS
ALL CITATIONS AVAILABLE IN TH[illegible]E FORMAT

L19 ANSWER 4 OF 17 CAPLUS COPYRIGHT 2001 ACS
AB We have identified 39 Arabidopsis thaliana ESTs encoding **germin**-like proteins (GLPs) and have completely sequenced 25 of these cDNAs. Our anal. demonstrates that the Arabidopsis genome contains a gene family with at least 12 GLP genes. Comparisons with other known germins and **germin**-like proteins indicate that these Arabidopsis GLP subfamilies are unique from wheat **germin**. All other known GLPs fall into one of these subfamilies. The translated GLPs show approx. 35% amino acid identity with other GLPs outside of their subfamily and significantly higher levels of identity within their resp. subfamily. The 3' ends of many of the GLP cDNAs are heterogeneous and several sites of polyadenylation are used. Ten of the GLPs have N-terminal signal sequences and most appear to be exported from the cell. Structurally, the GLPs are predicted to have a high content of .beta.-pleated sheet. Seven conserved regions of .beta.-sheet were found in each of the GLP proteins along with .alpha.-helixes located at both N- and C-termini. These same structural elements are also conserved in wheat **germin**. With one exception, all GLP family members contain at least one N-glycosylation site. All of these sites are conserved in an unstructured loop between .beta.-1 and .beta.-2. Genes for two of these GLPs were identified in genomic sequences previously deposited in the GenBank. The GLP3b gene is phys. linked to the polyubiquitin 4 gene. The 3' end of the GLP3b mRNA is only 0.5 kb from the ubq4 start of transcription. Anal. of the GLP3b **promoter** shows the presence of a single putative auxin-response sequence located at -124 to -111 upstream from the 5' end of the GLP3b mRNA. The GLP9 gene was identified in an Arabidopsis contig from Chromosome 4.

ACCESSION NUMBER: 1999:44295 CAPLUS
DOCUMENT NUMBER: 130:219004
TITLE: Arabidopsis thaliana contains a large family of germin-like proteins: characterization of cDNA and genomic sequences encoding 12 unique family members
AUTHOR(S): Carter, Clay; Graham, Richard A.; Thornburg, Robert W.
CORPORATE SOURCE: Department of Biochemistry and Biophysics, Iowa State University, Ames, IA, 50011, USA
SOURCE: Plant Mol. Biol. (1998), 38(6), 929-943
CODEN: PMBIDB; ISSN: 0167-4412
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 60
REFERENCE(S):
(2) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(3) Apostol, I; Plant Physiol 1989, V90, P109 CAPLUS
(5) Berget, S; Nature 1984, V309, P179 CAPLUS
(6) Bernier, F; Gene 1987, V59, P265 CAPLUS
(8) Bjellqvist, B; Electrophoresis 1993, V14, P1023 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L19 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2001 ACS
AB Wheat **germin** is a homopentameric 125 kD glycoprotein mainly localized in the cell wall of monocots, and is a specific marker of the onset of growth in germinating seeds. The major objective of this study was to examine the expression and oxalate oxidase activity of two wheat **germin** isoforms: gf-2.8 and gf 3.8 in transgenic tobacco plants. Transgenic tobacco plants were created with different constructs: (1) one entire excision of gf-2.8 **germin promoter** and two

partially delete[redacted]romoter sequences were used to [redacted]nerate 3 independent GUS [redacted]structs; (2) the whole gf-2.8 [redacted]e construct and the fusion with CaMV 35S **promoter**, (3) one entire excision of gf-3.8 **germin** gene and one partially deleted gf-3.8 **promoter** sequences were used to generate 2 independent GUS constructs; (4) the whole gf-3.8 gene and the fusion with CaMV 35S **promoter**. Hormonal treatment (auxin and gibberellin), salt treatment, heavy metals (Mn, Fe, Co, Ni, Cu, Zn, Cd, Hg, As) and Al induced high GUS activity in tobacco transformed with entire and one partially deleted of the gf-2.8 gene. The immunoblotting confirmed induction of gf-2.8 gene and its product expressed oxalate oxidase activity in tobacco transformed with the entire gf-2.8 construct. Neither nicotinic acid, salicylic acid, heat shock, cold nor UV-C have enhanced significant GUS activity and **germin** gf-2.8 synthesis and activity.

ACCESSION NUMBER: 1998:408950 CAPLUS
DOCUMENT NUMBER: 129:173106
TITLE: Gene expression and oxalate oxidase activity of two germin isoforms induced by stress
AUTHOR(S): Nowakowska, Justyna
CORPORATE SOURCE: I.B.M.P. C.N.R.S., Institut de Botanique, Universite Louis Pasteur, Strasbourg, 67083, Fr.
SOURCE: Acta Physiol. Plant. (1998), 20(1), 19-33
CODEN: APPLDE; ISSN: 0137-5881
PUBLISHER: Polish Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

L19 ANSWER 6 OF 17 CAPLUS COPYRIGHT 2001 ACS
AB Wheat (Triticum aestivum) **germin** is a homopentameric glycoprotein whose synthesis is allied with seed germination. **Germin** pentamers show an unusual resistance to dissocn. and possess an oxalate oxidase (OxO) activity. In order to increase our knowledge of **germin** gene expression, the function(s) of **germin** during development and possible uses in plant genetic engineering, an in vivo expression system is required. To this end, a gene for **germin**, named gf-2.8, was studied by expressing either **promoter**-GUS fusions or the intact gene in transgenic tobacco (Nicotiana tabacum) plants. Heterologous gene transcription was monitored in vitro and in vivo by GUS or OxO activity and was found to occur in developing seeds and in seedlings. This transcription was stimulated by auxins, as would be expected because of the presence of putative auxin-responsive elements in the **promoter** of the gf-2.8 gene. Auxin stimulation also extended to young leaves since OxO activity could be detected in treated but not in untreated leaves. The biochem. characteristics of wheat **germin** were also conserved in a transgenic host: the OxO activity was present under the form of a doublet co-migrating with **germin** G and G' isoforms. Also, **germin** distributed between a sol. and an apoplastic fractions despite the fact that wheat cell wall substantially differs from tobacco cell wall. Therefore, tobacco constitutes a suitable host for in vivo studies of this monocotyledon gene.

ACCESSION NUMBER: 1997:188905 CAPLUS
DOCUMENT NUMBER: 126:260065
TITLE: Regulated expression of a wheat germin gene in tobacco: oxalate oxidase activity and apoplastic localization of the heterologous protein
AUTHOR(S): Berna, Anne; Bernier, Francois
CORPORATE SOURCE: Institut de Botanique, I.B.M.P. du C.N.R.S., Universite Louis Pasteur, Strasbourg, 67083, Fr.
SOURCE: Plant Mol. Biol. (1997), 33(3), 417-429
CODEN: PMBIDB; ISSN: 0167-4412
PUBLISHER: Kluwer
DOCUMENT TYPE: Journal

LANGUAGE: English

L19 ANSWER 7 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS
AB In Arabidopsis thaliana, steady-state abundance of the Atger3 transcript encoding a **germin**-like cell wall protein follows a circadian rhythm, reaching its highest level at the beginning of the night. As a first step towards dissecting the molecular mechanisms underlying these transcript oscillations, the Atger3 genomic locus was characterised. Transcriptional fusions of 1.8 kb and 967 bp Atger3 **promoter** fragments to the beta-glucuronidase (GUS) reporter gene mediate high-amplitude circadian oscillations of the GUS transcript in transgenic Arabidopsis. 5' deletion to -490 greatly reduces overall transcript abundance while retaining a basal oscillation. Further deletion to -299 abolishes preferential GUS expression in the evening. Taken together, these data indicate that clock-response elements contributing to high-amplitude Atger3 oscillations largely reside between -299 and -967. Histochemical staining for GUS activity indicates that the Atger3 **promoter** is active in cotyledons, youngleaves, petioles, the inflorescence axis, pedicels, sepals, ovary, style and siliques but not in roots, petals and anthers.
ACCESSION NUMBER: 1999:455855 BIOSIS
DOCUMENT NUMBER: PREV199900455855
TITLE: The Atger3 promoter confers circadian clock-regulated transcription with peak expression at the beginning of the night.
AUTHOR(S): Staiger, Dorothee (1); Apel, Klaus; Trepp, Gian
CORPORATE SOURCE: (1) Institute for Plant Sciences, ETH Center, Swiss Federal Institute of Technology, 8092, Zurich Switzerland
SOURCE: Plant Molecular Biology, (July, 1999) Vol. 40, No. 5, pp. 873-882.
ISSN: 0167-4412.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L19 ANSWER 8 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS
AB Germins and **germin**-like proteins (GLPs) constitute a ubiquitous family of plant proteins that seem to be involved in many developmental and stress-related processes. Wheat **germin** has been extensively studied at the biochemical level: it is found in the apoplast and the cytoplasm of germinating embryo cells and it has oxalate oxidase activity (EC 1.2.3.4). **Germin** synthesis can also be induced in adult wheat leaves by auxins and by a fungal pathogen but it remains to be determined whether the same gene is involved in developmental, hormonal and stress response. In this work, we have studied the expression of one of the wheat **germin** genes, named gf-2.8, in wheat as well as in transgenic tobacco plants transformed with either this intact gene or constructs with GUS driven by its **promoter**. This has allowed us to demonstrate that expression of this single gene is both developmentally and pathogen-regulated. In addition, we show that expression of the wheat gf-2.8 **germin** gene is also stimulated by some abiotic stresses, especially the heavy metal ions Cd2+, Cu2+ and Co2+. Several chemicals involved in stress signal transduction pathways were also tested: only polyamines were shown to stimulate expression of this gene. Because regulation of the wheat gf-2.8 **germin** gene is complex and because its product results in developmental and stress-related release of hydrogen peroxide in the apoplast, it is likely that it plays an important role in several aspects of plant growth and defence mechanisms.
ACCESSION NUMBER: 1999:227007 BIOSIS
DOCUMENT NUMBER: PREV199900227007

TITLE: [redacted]ulation by biotic and abiotic [redacted]ess of a wheat germin [redacted]e encoding oxalate oxidase, a [redacted]2-producing enzyme.
AUTHOR(S): Berna, Anne; Bernier, Francois (1)
CORPORATE SOURCE: (1) Institut de Biologie Moleculaire des Plantes, Institut de Botanique, 28 rue Goethe, 67083, Strasbourg Cedex France
SOURCE: Plant Molecular Biology, (Feb., 1999) Vol. 39, No. 3, pp. 539-549.
ISSN: 0167-4412.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L19 ANSWER 9 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS
AB We have identified 39 Arabidopsis thaliana ESTs encoding **germin**-like proteins (GLPs) and have completely sequenced 25 of these cDNAs. Our analysis demonstrates that the Arabidopsis genome contains a gene family with at least 12 GLP genes. Comparisons with other known germins and **germin**-like proteins indicate that these Arabidopsis GLP subfamilies are unique from wheat **germin**. All other known GLPs fall into one of these subfamilies. The translated GLPs show approximately 35% amino acid identity with other GLPs outside of their subfamily and significantly higher levels of identity within their respective subfamily.
The 3' ends of many of the GLP cDNAs are heterogeneous and several sites of polyadenylation are used. Ten of the GLPs have N-terminal signal sequences and most appear to be exported from the cell. Structurally, the GLPs are predicted to have a high content of beta-pleated sheet. Seven conserved regions of beta-sheet were found in each of the GLP proteins along with alpha-helices located at both N- and C-termini. These same structural elements are also conserved in wheat **germin**. With one exception, all GLP family members contain at least one N-glycosylation site. All of these sites are conserved in an unstructured loop between beta-1 and beta-2. Genes for two of these GLPs were identified in genomic sequences previously deposited in the GenBank. The GLP3b gene is physically linked to the polyubiquitin 4 gene. The 3' end of the GLP3b mRNA is only 0.5 kb from the ubq4 start of transcription. Analysis of the GLP3b **promoter** shows the presence of a single putative auxin-response sequence located at -124 to -111 upstream from the 5' end of the GLP3b mRNA. The GLP9 gene was identified in an Arabidopsis contig from Chromosome 4.
ACCESSION NUMBER: 1999:86720 BIOSIS
DOCUMENT NUMBER: PREV199900086720
TITLE: Arabidopsis thaliana contains a large family of germin-like proteins: Characterization of cDNA and genomic sequences encoding 12 unique family members.
AUTHOR(S): Carter, Clay; Graham, Richard A.; Thornburg, Robert W. (1)
CORPORATE SOURCE: (1) 2212 Molecular Biol. Buil., Dep. Biochem. and Biophysics, Iowa State Univ. Ames, IA 50011 USA
SOURCE: Plant Molecular Biology, (Dec., 1998) Vol. 38, No. 6, pp. 929-943.
ISSN: 0167-4412.
DOCUMENT TYPE: Article
LANGUAGE: English

L19 ANSWER 10 OF 17 BIOSIS COPYRIGHT 2001 BIOSIS
AB Wheat **germin** is a homopentameric 125 kD glycoprotein mainly localized in the cell wall of monocots, and is a specific marker of the onset of growth in germinating seeds. The major objective of this study was to examine the expression and oxal ate oxidase activity of two wheat **germin** isoforms: gf-2.8 and gf-3.8 in transgenic tobacco plants. The transgenic tobacco plants were created with different constructs: 1)

one entire excision of gf-2.8 **germin promoter** and two partially deleted **promoter** sequences were used to generate 3 independent GUS constructs; 2) the whole gf-2.8 gene construct and the fusion with CaMV 35S **promoter**; 3) one entire excision of gf-3.8 **germin** gene and one partially deleted gf-3.8 **promoter** sequences were used to generate 2 independent GUS constructs; 4) the whole gf-3.8 gene and the fusion with CaMV 35S **promoter**. Hormonal treatment (auxin and gibberellin), salt treatment, heavy metals (Mn, Fe, Co, Ni, Cu, Zn, Cd, Hg, As) and Al induced high GUS activity in tobacco transformed with entire and one partially deleted of the gf-2.8 gene. The immunoblotting confirmed induction of gf-2.8 gene and its product expressed oxalate oxidase activity in tobacco transformed with the entire gf-2.8 construct. Neither nicotinic acid, salicylic acid, heat shock, cold nor UV-C have enhanced significant CUS activity and **germin** gf-2.8 synthesis and activity. The **germin** gf-3.8 constructs with CUS gene and with the entire gf-3.8 seguences gave non-positive response with factors mentioned above. It has been demonstrated that gf-3.8 **germin** isoform is present as a monomer (Mr 25 kD). The non-active gf-3.8 protein is synthetised in transgenic tobacco plants only under control of the CaMV 35S **promoter**. Consequently, among two **germin** isoforms, only the gf-2.8 protein seems to be regulated by hormonal, salt and heavy metal factors. The gf-2.8 oxalate oxidase activity could be then involved in general stress-induced signalling in plant.

ACCESSION NUMBER: 1998:324537 BIOSIS
DOCUMENT NUMBER: PREV199800324537
TITLE: Cene expression and oxalate oxidase activity of two germin isoforms induced by stress.
AUTHOR(S): Nowakowska, Justyna (1)
CORPORATE SOURCE: (1) Dep. Environ. Prot., Warsaw Agric. Univ.-SCCW, Nowoursynowska 166, 02-766 Warsaw Poland
SOURCE: Acta Physiologiae Plantarum, (1998) Vol. 20, No. 1, pp. 19-33.
ISSN: 0137-5881.
DOCUMENT TYPE: Article
LANCUACE: English

=> d his

(FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001

L1	1274	S	MALATE(W)SYNTHASE
L2	199155	S	PROMOTER
L3	203	S	CERMIN
L4	877	S	CLYOXYSOMAL
L5	0	S	ALEUTRONE(W)LAYER
L6	0	S	ALEUTRONE
L7	13735	S	CARBOXYPEPTIDASE
L8	8459	S	GLUTATHIONE(W)TRANSFERASE
L9	478	S	ALCA
L10	186	S	ALCR
L11	0	S	IACC(P)REPRESSOR
L12	13	S	IACC
L13	6132	S	434
L14	4174	S	P22
L15	3352	S	TET
L16	21064	S	REPRESSOR
L17	459	S	LAMBDA(W)BACTERIOPHACE
L18	44	S	L1(P)L2
L19	17	S	L3(P)L2

```
L20          14 S L4[redacted]L2
L21         170 S L7[redacted]L2
L22          72 S L8(P)L2
L23          84 S L9(P)L2
L24          36 S L10(P)L2
L25           0 S L12(P)L2
L26         356 S L13(P)L16
L27         289 S L14(P)L16
L28         419 S L15(P)L16
L29          12 S L17(P)L16

=> d l20 1-10 abs ibib


L20  ANSWER 1 OF 14  CAPLUS  COPYRIGHT 2001 ACS
AB   Glyoxysomal 3-ketoacyl-CoA thiolase is the last enzyme in the
     .beta.-oxidn. of fatty acids in plant glyoxysomes.  A full-length cDNA of
     the glyoxysomal 3-ketoacyl-CoA thiolase from Brassica napus and
     a truncated version, lacking the N-terminal targeting signal were cloned
     in a T7 promoter-based vector.  Both recombinant proteins were
     expressed in Escherichia coli and activity was measured.  Full-length and
     truncated 3-ketoacyl-CoA thiolase have comparable activity in E. coli.
     Moreover, full-length 3-ketoacyl-CoA thiolase was purified from E. coli
     and N-terminal sequencing of the protein confirmed that the precursor
form
     indeed is enzymically active.
ACCESSION NUMBER:         1997:469576  CAPLUS
DOCUMENT NUMBER:          127:216945
TITLE:                    The glyoxysomal 3-ketoacyl-CoA thiolase precursor
from
                          Brassica napus has enzymic activity when synthesized
                          in Escherichia coli
AUTHOR(S):                Olesen, Christian; Thomsen, Karl Kristian; Svendsen,
                          Ib; Brandt, Anders
CORPORATE SOURCE:         Department of Physiology, Carlsberg Laboratory, Gamle
                          Carlsbergvej 10, Copenhagen Valby, DK-2500, Den.
SOURCE:                   FEBS Lett. (1997), 412(1), 138-140
                          CODEN: FEBLAL; ISSN: 0014-5793
PUBLISHER:                Elsevier
DOCUMENT TYPE:            Journal
LANGUAGE:                 English

L20  ANSWER 2 OF 14  CAPLUS  COPYRIGHT 2001 ACS
AB   A cDNA coding for radish (Raphanus sativus L.) acetoacetyl-CoA thiolase
     (AACT) was cloned by complementation of the erg10 mutation affecting AACT
     in yeast (Saccharomyces cerevisiae).  The longest reading frame encodes a
     protein of 406 amino acids with a predicted relative mol. wt. of 42,032,
     with significant similarities to eukaryotic and prokaryotic thiolases.
     There is no evidence for the presence of a leader peptide characteristic,
     e.g. of glyoxysomal thiolase.  Yeast transformants expressing
     the radish AACT gene placed under the control of the GAL1 promoter
     exhibited a 10-fold higher enzyme activity than a wild-type yeast strain
     after induction by galactose.  This enzyme activity is exclusively
     localized in the sol. fraction but not in membranes.  These data indicate
     that we have cloned a gene encoding cytoplasmic (biosynthetic) AACT.
     Genomic DNA gel blot anal. suggests the presence of a single AACT gene,
     which is expressed in all parts of the seedling.  Expression in
cotyledons
     appears to be light-stimulated.  We present preliminary evidence that a
     smaller transcript represents an antisense species being read from the
     same gene.
ACCESSION NUMBER:         1996:505355  CAPLUS
DOCUMENT NUMBER:          125:187093
TITLE:                    Cloning of a cDNA encoding cytosolic
                          acetoacetyl-coenzyme A thiolase from radish by
```

functional expression in Sac[redacted]romyces cerevisiae
AUTHOR(S): Vollack, Kai-Uwe; Bach, Thom[redacted]J.
CORPORATE SOURCE: Botanisches Inst. II, Univ. Karlsruhe, Karlsruhe, D-76128, Germany
SOURCE: Plant Physiol. (1996), 111(4), 1097-1107
CODEN: PLPHAY; ISSN: 0032-0889
DOCUMENT TYPE: Journal
LANGUAGE: English

L20 ANSWER 3 OF 14 CAPLUS COPYRIGHT 2001 ACS
AB We analyzed DNA seguences that regulate the expression of an isocitrate lyase gene from Brassica napus L. during late embryogenesis and during postgerminative growth to det. whether **glyoxysomal** function is induced by a common mechanism at different developmental stages. .beta.-Glucuronidase constructs were used both in transient expression assays in B. napus and in transgenic Arabidopsis thaliana to identify the segments of the isocitrate lyase 5' flanking region that influence **promoter** activity. DNA seguences that play the principal role in activating the **promoter** during post-germinative growth are located more than 1200 bp upstream of the gene. Distinct DNA sequences that were sufficient for high-level expression during late embryogenesis but only low-level expression during postgerminative growth were also identified. Other parts of the 5' flanking region increased **promoter** activity both in developing seed and in seedlings. We conclude that a combination of elements is involved in regulating the isocitrate lyase gene and that distinct DNA seguences play primary roles in the activating the gene in embryos and in seedlings. These findings suggest that different signals contribute to the induction of **glyoxysomal** function during these two developmental stages. We also showed that some of the constructs were expressed differently in transient expression assays and in transgenic plants.
ACCESSION NUMBER: 1996:231037 CAPLUS
DOCUMENT NUMBER: 124:309319
TITLE: DNA seguences that activate isocitrate lyase gene expression during late embryogenesis and during postgerminative growth
AUTHOR(S): Zhang, James Z.; Santes, Cristina M.; Engel, Michele L.; Gasser, Charles S.; Harada, John J.
CORPORATE SOURCE: Div. Biological Sciences, Univ. California, Davis, CA,
95616, USA
SOURCE: Plant Physiol. (1996), 110(4), 1069-79
CODEN: PLPHAY; ISSN: 0032-0889
DOCUMENT TYPE: Journal
LANGUAGE: English

L20 ANSWER 4 OF 14 CAPLUS COPYRIGHT 2001 ACS
AB Two main types of peroxisomal targeting signals have been identified that reside either at the extreme C terminus (PTS1) or the N terminus (PTS2) of
the protein. In the methylotrophic yeast hansenula polymorpha the majority of peroxisomal matrix proteins are of the PTS1 type. Thus far, for H. polymorpha only amine oxidase (AMO) has been shown to contain a PTS2 type signal. In the present study we expressed H. polymorpha AMO under control of the strong endogenous alc. oxidase **promoter**. Partial import of AMO into peroxisomes was obsd. in cells grown in methanol/(NH4)2SO4-contg. medium. However, complete import of AMO occurred if the cells were grown under conditions that induce expression of the endogenous AMO gene. Similar results were obtained when the heterologous PTS2 proteins, **glyoxysomal** malate dehydrogenase from watermelon and thiolase from Saccharomyces cerevisiae, were synthesized in H. polymorpha. The import of PTS1 proteins, however, was not affected by the growth conditions. These results indicate that the reduced rate of AMO import in (NH4)2SO4-grown cells is not due to competition with PTS1 proteins for the same import pathway. Apparently,

AMO is imported via a sep. pathway that is induced by amines and functions
for PTS2 proteins in general.
ACCESSION NUMBER: 1995:284936 CAPLUS
DOCUMENT NUMBER: 122:51016
TITLE: The methylotrophic yeast Hansenula polymorpha contains
an inducible import pathway for peroxisomal matrix proteins with an N-terminal targeting signal (PTS2 proteins)
AUTHOR(S): Faber, Klaas Nico; Haima, Peter; Gietl, Christine; Harder, Wim; AB, Geert; Veenhuis, Marten
CORPORATE SOURCE: Lab. Electron Microscopy, Univ. Groningen, Haren, 9751
NN, Neth.
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1994), 91(26), 12985-9
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

L20 ANSWER 5 OF 14 CAPLUS COPYRIGHT 2001 ACS
AB The fate of the watermelon (Citrullus vulgaris Schrad.) **glyoxysomal** enzyme, malate dehydrogenase (gMDH), after synthesis in the methylotrophic yeast, H. polymorpha, was studied. The gene encoding the precursor form of gMDH (pre-gMDH) was cloned in an H. polymorpha expression vector downstream of the inducible H. polymorpha alc. oxidase **promoter**. During methylotrophic growth, pre-gMDH was synthesized and imported into peroxisomes, where it was enzymically active. The apparent mol. wt. of the protein located in H. polymorpha peroxisomes was equal to that of pre-gMDH (41 kDa), indicating that N-terminal processing of the transit peptide had not occurred in the yeast.
ACCESSION NUMBER: 1994:27175 CAPLUS
DOCUMENT NUMBER: 120:27175
TITLE: Watermelon glyoxysomal malate dehydrogenase is sorted to peroxisomes of the methylotrophic yeast, Hansenula polymorpha
AUTHOR(S): der Klei, I. J. van; Faber, K. N.; Keizer-Gunnink, I.;
Gietl, C.; Harder, W.; Veenhuis, M.
CORPORATE SOURCE: Laboratory for Electron Microscopy, Biological Centre,
University of Groningen, Kerklaan 30, NN Haren, 9751, Neth.
SOURCE: FEBS Lett. (1993), 334(1), 128-32
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English

L20 ANSWER 6 OF 14 CAPLUS COPYRIGHT 2001 ACS
AB The cDNA encoding castor bean endosperm isocitrate lyase (ICL) was expressed under the control of the promoter of the small subunit of pea ribulose bisphosphate carboxylase in transformed tobacco. ICL protein was
detected using anti-ICL antibodies on immunoblots of total leaf protein exts. Nycodenz d. gradient sepn. of the exts. from the transgenic tobacco
leaves showed ICL co-fractionated with hydroxypyruvate reductase, a peroxisomal matrix marker protein, and away from lactate dehydrogenase, a cytosolic marker protein. Immunoelectron microscopy of ultrathin leaf sections demonstrated the location of ICL within the matrix of the leaf peroxisomes of the transgenic plants. In vitro transcribed and translated
ICL was also imported into leaf peroxisomes isolated from germinating

sunflower seeds. The in vivo and in vitro import of this protein into leaf peroxisomes provides strong support for the notion that the import machinery of glyoxysomes and peroxisomes is very similar.

ACCESSION NUMBER: 1993:599638 CAPLUS
DOCUMENT NUMBER: 119:199638
TITLE: Targeting of castor bean glyoxysomal isocitrate lyase to tobacco leaf peroxisomes
AUTHOR(S): Onyeocha, I.; Behari, R.; Hill, D.; Baker, A.
CORPORATE SOURCE: Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK
SOURCE: Plant Mol. Biol. (1993), 22(3), 385-96
CODEN: PMBIDB; ISSN: 0167-4412
DOCUMENT TYPE: Journal
LANGUAGE: English

L20 ANSWER 7 OF 14 BIOSIS COPYRIGHT 2001 BIOSIS
AB **Glyoxysomal** 3-ketoacyl-CoA thiolase is the last enzyme in the beta-oxidation of fatty acids in plant glyoxysomes. A full-length cDNA of the **glyoxysomal** 3-ketoacyl-CoA thiolase from Brassica napus and a truncated version, lacking the N-terminal targeting signal were cloned in a T7 **promoter**-based vector. Both recombinant proteins were expressed in Escherichia coli and activity was measured. Full-length and truncated 3-ketoacyl-CoA thiolase have comparable activity in E. coli. Moreover, full-length 3-ketoacyl-CoA thiolase was purified from E. coli and N-terminal sequencing of the protein confirmed that the precursor form indeed is enzymatically active.

ACCESSION NUMBER: 1997:398352 BIOSIS
DOCUMENT NUMBER: PREV199799697555
TITLE: The glyoxysomal 3-ketoacyl-CoA thiolase precursor from Brassica napus has enzymatic activity when synthesized in Escherichia coli.
AUTHOR(S): Olesen, Christian; Thomsen, Karl Kristian; Svendsen, Ib; Brandt, Anders (1)
CORPORATE SOURCE: (1) Dep. Physiol., Carlsberg Lab., Gamle Carlsbergvej 10, DK-2500 Copenhagen Valby Denmark
SOURCE: FEBS Letters, (1997) Vol. 412, No. 1, pp. 138-140. ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English

L20 ANSWER 8 OF 14 BIOSIS COPYRIGHT 2001 BIOSIS
AB A cDNA coding for radish (Raphanus sativus L.) acetoacetylcoenzyme A thiolase (AACT) was cloned by complementation of the erg10 mutation affecting AACT in yeast (Saccharomyces cerevisiae). The longest reading frame encodes a protein of 406 amino acids with a predicted relative molecular weight of 42,032, with significant similarities to eukaryotic and prokaryotic thiolases. There is no evidence for the presence of a leader peptide characteristic, e.g. of **glyoxysomal** thiolase. Yeast transformants expressing the radish AACT gene placed under the control of the GAL1 **promoter** exhibited a 10-fold higher enzyme activity than a wild-type yeast strain after induction by galactose. This enzyme activity is exclusively localized in the soluble fraction but not in membranes. These data indicate that we have cloned a gene encoding cytoplasmic (biosynthetic) AACT. Genomic DNA gel blot analysis suggests the presence of a single AACT gene, which is expressed in all parts of the seedling. Expression in cotyledons appears to be light-stimulated. We present preliminary evidence that a smaller transcript represents an antisense species being read from the same gene.

ACCESSION NUMBER: 1996:462581 BIOSIS
DOCUMENT NUMBER: PREV199699184937
TITLE: Cloning of a cDNA encoding cytosolic acetoacetyl-coenzyme A thiolase from radish by functional expression in

charomyces cerevisiae.
AUTHOR(S): [redacted]lack, Kai-Uwe; Bach, Thomas J.[redacted])
CORPORATE SOURCE: (1) Centre Natl. de la Recherche Scientifique, Inst. de Biologie Moleculaire des Plantes, Dep. d'Enzymologie Cellulaire et Moleculaire, Inst. de Botanique, Univ. Louis Pasteur, F-67083 Strasbourg France
SOURCE: Plant Physiology (Rockville), (1996) Vol. 111, No. 4, pp. 1097-1107.
ISSN: 0032-0889.
DOCUMENT TYPE: Article
LANGUAGE: English

L20 ANSWER 9 OF 14 BIOSIS COPYRIGHT 2001 BIOSIS
AB We analyzed DNA sequences that regulate the expression of an isocitrate lyase gene from Brassica napus L. during late embryogenesis and during postgerminative growth to determine whether **glyoxysomal** function is induced by a common mechanism at different developmental stages. beta-Glucuronidase constructs were used both in transient expression assays in B. napus and in transgenic Arabidopsis thaliana to identify the segments of the isocitrate lyase 5' flanking region that influence **promoter** activity. DNA sequences that play the principal role in activating the **promoter** during postgerminative growth are located more than 1200 hp upstream of the gene. Distinct DNA sequences that were sufficient for high-level expression during late embryogenesis but only low-level expression during postgerminative growth were also identified. Other parts of the 5' flanking region increased **promoter** activity both in developing seed and in seedlings. We conclude that a combination of elements is involved in regulating the isocitrate lyase gene and that distinct DNA sequences play primary roles in activating the gene in embryos and in seedlings. These findings suggest that different signals contribute to the induction of **glyoxysomal** function during these two developmental stages. We also showed that some of the constructs were expressed differently in transient expression assays and in transgenic plants.
ACCESSION NUMBER: 1996:268108 BIOSIS
DOCUMENT NUMBER: PREV199698824237
TITLE: DNA sequences that activate isocitrate lyase gene expression during late embryogenesis and during postgerminative growth.
AUTHOR(S): Zhang, James Z.; Santes, Cristina M.; Engel, Michele L.; Gasser, Charles S.; Harada, John J. (1)
CORPORATE SOURCE: (1) Sections Plant Biol., Div. Biol. Sci., Univ. California, Davis, CA 95616 USA
SOURCE: Plant Physiology (Rockville), (1996) Vol. 110, No. 4, pp. 1069-1079.
ISSN: 0032-0889.
DOCUMENT TYPE: Article
LANGUAGE: English

L20 ANSWER 10 OF 14 BIOSIS COPYRIGHT 2001 BIOSIS
AB Two main types of peroxisomal targeting signals have been identified that reside either at the extreme C terminus (PTS1) or the N terminus (PTS2) of the protein. In the methylotrophic yeast Hansenula polymorpha the majority of peroxisomal matrix proteins are of the PTS1 type. Thus far, for H. polymorpha only amine oxidase (AMO) has been shown to contain a PTS2 type signal. In the present study we expressed H. polymorpha AMO under control of the strong endogenous alcohol oxidase **promoter**. Partial import of AMO into peroxisomes was observed in cells grown in methanol/(NH-4)-2SO-4-containing medium. However, complete import of AMO occurred if the cells were grown under conditions that induce expression of the endogenous AMO gene. Similar results were obtained when the heterologous PTS2 proteins, **glyoxysomal** malate dehydrogenase

from watermelon and thiolase from Saccharomyces cerevisiae, were synthesized in H. polymorpha. The import of PTS1 proteins, however, was not affected by the growth conditions. These results indicate that the reduced rate of AMO import in (NH-4)-2SO-4-grown cells is not due to competition with PTS1 proteins for the same import pathway. Apparently, AMO is imported via a separate pathway that is induced by amines and functions for PTS2 proteins in general.

ACCESSION NUMBER: 1995:69441 BIOSIS
DOCUMENT NUMBER: PREV199598083741
TITLE: The methylotrophic yeast Hansenula polymorpha contains an inducible import pathway for peroxisomal matrix proteins with an N-terminal targeting signal (PTS2 proteins.
AUTHOR(S): Faber, Klaas Nico; Haima, Peter; Gietl, Christine; Harder, Wim; Ab, Geert; Veenhuis, Marten (1)
CORPORATE SOURCE: (1) Lab. Electron Microscopy, Biol. Centre, University Groningen, Kerklaan 30, 9751 NN Haren Netherlands
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1994) Vol. 91, No. 26, pp. 12985-12989.
ISSN: 0027-8424.
DOCUMENT TYPE: Article
LANGUAGE: English

=> d l21 1-10 abs ibib

L21 ANSWER 1 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB A DNA encoding a fusion protein of formula (1) comprising a leader peptide sequence (Y) consisting of at least one amino acid residue for the expression and secretion of the protein, an amino acid sequence (X1) to be used in enzymic or chem. cleavage, an amino acid sequence (B-chain) of insulin B chain, an amino acid sequence (X2) to be used in enzymic cleavage, a linker sequence (Linker) consisting of at least one amino acid residue, an amino acid sequence (X3) to be used in enzymic cleavage, and an amino acid sequence (A-chain) of insulin A chain, which are linked to each other in this order; and a process for producing insulin by using an expression system contg. this DNA, are disclosed.: [Y]-[X1]-[B-chain]-[X2]-[Linker]-[X3]-[A-chain] (Formula I). Thus, a process for efficiently producing gene recombinant insulin at a high productivity is provided. The amino acid sequences X1, X2, and X3 used in enzymic cleavage is comprised of thrombin cleavage sites. The leader peptide comes from Bacillus cell wall protein (CWP), middle wall protein (MWP) N-terminal 9 amino acid sequence. Addn. of CWP signal peptide to the 5' of DNA sequence in Formula I is claimed. Use of a **promoter** region necessary for the recombinant fusion protein expression in prokaryote or eukaryote, preferably of Bacillus CWP origin, is also claimed. Expression in Bacillus, Bacillus brevis in particular, is claimed. Enzymic cleavage by thrombin and **carboxypeptidase** B is used. Recombinant insulin produced with this method showed blood glucose lowering effect comparable to that of another recombinant insulin.

ACCESSION NUMBER: 2000:790637 CAPLUS
DOCUMENT NUMBER: 133:359778
TITLE: Recombinant insulin production from enzymic cleavage of novel fusion protein
INVENTOR(S): Oka, Shusaku; Sato, Seiji; Higashikuni, Naohiko; Kondo, Masaaki; Kudo, Toshiyuki; Watanabe, Shigeaki; Waki, Yoshihiro; Yuki, Hirotaka
PATENT ASSIGNEE(S): Itoham Foods Inc., Japan
SOURCE: PCT Int. Appl., 54 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000066738	A1	20001109	WO 2000-JP2736	20000426
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
JP 2000316579	A2	20001121	JP 1999-124877	19990430

PRIORITY APPLN. INFO.: JP 1999-124877 19990430
REFERENCE COUNT: 28
REFERENCE(S):
(1) Eli Lilly And Company; GB 2072680 A CAPLUS
(2) Eli Lilly And Company; EP 37256 A CAPLUS
(3) Eli Lilly And Company; JP 56154443 A 1981 CAPLUS
(4) Higeta Shoyu Co Ltd; JP 06253862 A 1994 CAPLUS
(5) Hoechst Aktiengesellschaft; DE 3936876 A CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 2 OF 170 CAPLUS COPYRIGHT 2001 ACS

AB Disclosed are Hansenula polymorpha mutants useful as host cells through which various proteins can be produced as being intact at high yield and a process for prepg. recombinant proteins using the host cells. Using various vectors, Hansenula polymorpha is made to be a mutant which is deprived of methanol assimilating ability and incapable of utilizing methanol as a carbon source. This Hansenula polymorpha mutant is used as a high yield host to produce recombinant proteins without continuous feeding of methanol, with the aid of an expression cassette carrying a **promoter** capable of inducing the expression at a low concn. of methanol. Further, the mutant is also lacking in **carboxypeptidase** Y, protease Y and/or **carboxypeptidase** .alpha. activity, so the recombinant protein of interest is not degraded at its carboxyl terminal when being expressed in the cell. Thus, intact recombinant protein can be obtained. Also, there is disclosed a pop-out technique in which a recombinant protein expression cassette is inserted into a MOX gene site of the mutant and is allowed to pop out therefrom, thereby utilizing the mutant as a host for general use in producing various proteins of interest.

ACCESSION NUMBER: 2000:628241 CAPLUS
DOCUMENT NUMBER: 133:218506
TITLE: Hansenula polymorpha mutants unable to utilize methanol and deficient in proteinases and their use as expression hosts
INVENTOR(S): Rhee, Sangki; Choi, Euisung; Kang, Hyunah; Sohn, Junghoon; Bae, Junghoon; Kim, Moowoong; Agaphonov, Michael; Kim, Myungkuk
PATENT ASSIGNEE(S): Korea Research Institute of Bioscience and Biotechnology, S. Korea; Dong Kook Pharmaceutical Co.
SOURCE: PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000052133	A2	20000908	WO 2000-KR173	20000304

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ

RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: KR 1999-7177 19990304
KR 2000-10743 20000303

L21 ANSWER 3 OF 170 CAPLUS COPYRIGHT 2001 ACS

AB In the course of studying **carboxypeptidase** Y (CPY) prodn., we found that the expression level of the gene, which is under the control of the GAL10 **promoter**, increased in a Saccharomyces cerevisiae gal80 mutant grown in a medium contg. ethanol as the sole carbon source. In the cultivation of the gal80 mutant KS58-2D/pCY303 carrying a multicopy plasmid, which contains the PRC1 gene fused to the GAL10 **promoter**, CPY prodn. continued after the consumption of galactose. In this phase, the cells utilized ethanol as the carbon source. To increase the CPY prodn. level, the effect of carbon source feeding in a fed-batch culture were examd. The prodn. level in the fed-batch culture using ethanol was 1.3-fold higher than that in a batch culture and 1.6-fold higher than that in a fed-batch culture using galactose. By 5'-deletion anal. of the GAL10 **promoter**, the region between -256 and -232 was found to be important for the **promoter** activity in the gal80 mutant growing in the presence of ethanol.

ACCESSION NUMBER: 2000:472396 CAPLUS
DOCUMENT NUMBER: 133:206828
TITLE: Effect of ethanol on the production of **carboxypeptidase** Y using the GAL10 **promoter** in a Saccharomyces cerevisiae gal80 mutant
AUTHOR(S): Shiba, Yoichiro; Ono, Chiho; Fukui, Fumio; Yoshikawa, Hiroji
CORPORATE SOURCE: Lead Discovery Research Laboratories, Sankyo Co. Ltd., Fukushima, 971-8183, Japan
SOURCE: J. Biosci. Bioeng. (2000), 89(5), 426-430
CODEN: JBBIF6; ISSN: 1389-1723
PUBLISHER: Society for Bioscience and Bioengineering, Japan
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 26
REFERENCE(S):
(1) Baker, H; Proc Natl Acad Sci USA 1991, V88, P9443 CAPLUS
(2) Breddam, K; Carlsberg Res Commun 1987, V52, P55 CAPLUS
(3) Chasman, D; Genes Dev 1990, V4, P503 CAPLUS
(4) Chen, S; Genetics 1993, V134, P701 CAPLUS
(5) Finley, R; Mol Cell Biol 1989, V9, P4282 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 4 OF 170 CAPLUS COPYRIGHT 2001 ACS

AB Glycopeptide-resistant enterococci of the VanC type synthesize

UDP-muramyl-pe[redacted]eptide[D-Ser] for cell wall as[redacted]bly and prevent synthesis of pe[redacted]doglycan precursors ending in [redacted]Ala. The vanC cluster of Enterococcus gallinarum BM4174 consists of five genes: vanC-1, vanXYC, vanT, vanRC, and vanSC. Three genes are sufficient for resistance: vanC-1 encodes a ligase that synthesizes the dipeptide D-Ala-D-Ser for addn. to UDP-MurNAc-tripeptide, vanXYC encodes a D,D-dipeptidase-**carboxypeptidase** that hydrolyzes D-Ala-D-Ala and removes D-Ala from UDP-MurNAc-pentapeptide[D-Ala], and vanT encodes a membrane-bound serine racemase that provides D-Ser for the synthetic pathway. The three genes are clustered: the start codons of vanXYC and vanT overlap the termination codons of vanC-1 and vanXYC, resp. Two genes which encode proteins with homol. to the VanS-VanR two-component regulatory system were present downstream from the resistance genes. The predicted amino acid sequence of VanRC exhibited 50% identity to VanR and 33% identity to VanRB. VanSC had 40% identity to VanS over a region of 308 amino acids and 24% identity to VanSB over a region of 285 amino acids. All residues with important functions in response regulators and histidine kinases were conserved in VanRC and VanSC, resp. Induction expts. based on the detn. of D,D-**carboxypeptidase** activity in cytoplasmic exts. confirmed that the genes were expressed constitutively. Using a **promoter** -probing vector, regions upstream from the resistance and regulatory genes were identified that have **promoter** activity.

ACCESSION NUMBER: 2000:367612 CAPLUS
DOCUMENT NUMBER: 133:277022
TITLE: vanC cluster of vancomycin-resistant Enterococcus gallinarum BM4174
AUTHOR(S): Arias, Cesar A.; Courvalin, Patrice; Reynolds, Peter E.
CORPORATE SOURCE: Department of Biochemistry, University of Cambridge, Cambridge, UK
SOURCE: Antimicrob. Agents Chemother. (2000), 44(6), 1660-1666
CODEN: AMACCQ; ISSN: 0066-4804
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 44
REFERENCE(S):
(1) Altschul, S; Nucleic Acids Res 1997, V25, P3389 CAPLUS
(2) Arias, C; Mol Microbiol 1999, V31, P1653 CAPLUS
(3) Arthur, M; Antimicrob Agents Chemother 1994, V38, P1899 CAPLUS
(4) Arthur, M; Gene 1991, V103, P133 CAPLUS
(5) Arthur, M; J Bacteriol 1992, V174, P2582 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 5 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB The adipocyte-enhancer binding protein (AEBP) 1 is a novel transcriptional repressor with **carboxypeptidase** (CP) activity. AEBP1 binds to a regulatory sequence (termed adipocyte enhancer 1, AE-1) located in the proximal **promoter** region of the adipose P2 (aP2) gene, which encodes the adipocyte fatty-acid binding protein. Sequence comparisons and kinetic studies using known **carboxypeptidase** substrates, activators and inhibitors have characterized AEBP1 as a member of the regulatory B-like CP family. Significantly, the inherent CP activity of AEBP1 is stimulated by the AE-1 sequence. Our results indicate that AEBP1 is activated by a novel mechanism, whereby the direct binding of DNA enhances its protease activity. These results represent the first demonstration of DNA-mediated regulation of CP activity.

ACCESSION NUMBER: 1999:714146 CAPLUS
DOCUMENT NUMBER: 132:32571
TITLE: Enzymic characterization of a novel member of the regulatory B-like carboxypeptidase with transcriptional repression function: stimulation of enzymic activity by its target DNA
AUTHOR(S): Muise, Aleixo M.; Ro, Hyo-Sung
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Faculty of Medicine, Dalhousie University, Halifax, NS, B3H 4H7, Can.
SOURCE: Biochem. J. (1999), 343(2), 341-345
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 25
REFERENCE(S):
(2) Barabe, J; Biochem Pharmacol 1991, V41, P821 CAPLUS
(4) Christianson, D; Proc Natl Acad Sci 1987, V84, P1512 CAPLUS
(6) Deddish, P; J Biol Chem 1990, V265, P15083 CAPLUS
(7) Distel, R; Cell 1987, V49, P835 CAPLUS
(10) Fricker, L; Ann Rev Physiol 1988, V50, P309 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 6 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB Bacteriophage T7 lysozyme binds to T7 RNA polymerase (RNAP) and regulates its transcription by differentially repressing initiation from different T7 promoters. This selective repression is due in part to a lysozyme-induced increase in the KNTP of the initiation complex (IC) and to intrinsically different NTP concn. requirements for efficient initiation from different T7 promoters. While lysozyme represses initiation, once the enzyme has left the **promoter** and formed an elongation complex (EC) it is generally resistant to the effects of lysozyme. The mechanism by which the inhibitory effects of lysozyme are largely restricted to the initiation phase of transcription is not well understood. We find that T7 lysozyme destabilizes initial transcription complexes (ITCs) and increases the rate of release of transcripts from these complexes but does not destabilize ECs. However, if the RNA:RNAP interaction proposed to be important for EC stability is disrupted by proteolysis of the RNA-binding domain or use of templates which interfere with establishment of this RNA:RNAP interaction, the EC becomes sensitive to lysozyme. Comparison of the X-ray structures of T7RNAP and of a T7RNAP:T7 lysozyme complex reveals that lysozyme causes the C terminus of the polymerase to flip out of the active site. Expts. in which **carboxypeptidase** A is used to probe the lysozyme-induced exposure of the C terminus reveal a large decrease in **carboxypeptidase** sensitivity following transcription initiation, suggesting that interactions with the 3'-end of the RNA help stabilize the active site in a functional (**carboxypeptidase** protected) conformation. Thus, the resistance of the EC to lysozyme appears to be due to the consecutive establishment of two sets of RNA:RNAP interactions. The first is made with the 3'-end of the RNA and helps stabilize a functional conformation of the active site, thereby suppressing the effects of lysozyme on KNTP. The second is made with a more upstream element of the RNA and keeps the EC from being destabilized by lysozyme binding. (c) 1999 Academic Press.
ACCESSION NUMBER: 1999:697404 CAPLUS
DOCUMENT NUMBER: 132:74398
TITLE: Mechanisms by which T7 Lysozyme Specifically Regulates
T7 RNA Polymerase during Different Phases of Transcription
AUTHOR(S): Huang, Jianbin; Villemain, Jana; Padilla, Robert; Sousa, Rui

CORPORATE SOURCE: [redacted] Department of Biochemistry, [redacted]versity of Texas Health
Sciences Center, San Antonio, TX, 78284-7760, USA
SOURCE: J. Mol. Biol. (1999), 293(3), 457-475
CODEN: JMOBAK; ISSN: 0022-2836
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 44
REFERENCE(S): (1) Axelrod, V; Biochemistry 1985, V24, P5716 CAPLUS
(4) Cheetham, G; Nature 1999, V399, P80 CAPLUS
(5) Diaz, G; Biochemistry 1996, V35, P10837 CAPLUS
(6) Gardner, L; Biochemistry 1997, V36, P2908 CAPLUS
(8) Gross, L; J Mol Biol 1992, V228, P488 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 7 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB A method of manufg. a protein that increases the yield of correctly folded proteins by synthesizing it as a fusion protein with a peptide that promotes correct folding is described. The protein may be a chaperonin or a propeptide, e.g. from human growth hormone, that also helps to promote correct folding. The protein manufd. by an expression host is denatured with a chaotropic agent and allowed to renature with the chaperonin helping to direct correct folding. The chaperonin moiety can be removed by chem. cleavage. The method is particularly intended for use in the manuf. of insulin. An assay for screening an amino acid sequence for the ability to improve folding of an insulin precursor using a chimeric protein contg. an IMC like sequence linked to an insulin precursor is also described. Use of the human growth hormone propeptide to manuf. a human mini-proinsulin in Escherichia coli is demonstrated. Inclusion bodies contg. the protein were solubilized with alk. urea and renatured with a yield of .apprx.70%. The refolded material was purified by ultrafiltration with a yield of 85%. The insulin was released from the fusion protein with trypsin and the C-terminal arginine of the B chain was removed with carboxypeptidase. Cryst. insulin obtained from this stage had a purity of >99%.
ACCESSION NUMBER: 1999:640887 CAPLUS
DOCUMENT NUMBER: 131:267960
TITLE: Manufacture of proteins as fusion products with peptides that promoter protein folding and the manufacture of correctly-folded proteins
INVENTOR(S): Gan, Zhongru
PATENT ASSIGNEE(S): Tonghua Gantech Biotechnology Ltd., Peop. Rep. China
SOURCE: PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9950302	A1	19991007	WO 1998-CN52	19980331

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

AU 9867164 A1 19991018 AU 1998-67 19980331
BR 9815788 A 20001128 BR 1998-15 19980331
EP 1066328 A1 20010110 EP 1998-912192 19980331
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
PRIORITY APPLN. INFO.: WO 1998-CN52 19980331
REFERENCE COUNT: 2
REFERENCE(S): (1) Bio-Technology General Corp; WO 9620724 1996 CAPLUS
(2) Pharmacia & Upjohn Ab; WO 9718233 1997 CAPLUS

L21 ANSWER 8 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB A fusion gene encoding Met-Lys-double-C peptide human proinsulin was constructed with PCR. The mutation in it was confirmed by DNA sequencing, and it was expressed in E. coli system in inclusion body form. The temp. inducible **promoter** was employed for induction in a short time. After reducing and refolding, expressed recombinant products could be easily purified by Sephadex G-75 chromatog. The Met-Lys-double-C peptide human proinsulin analog could be changed into human insulin with the treatment of trypsin and **carboxypeptidase** B. After sepn. with anion exchange chromatog. Resource Q column, human insulin could be obtained. Polyacrylamide gel electrophoresis anal. showed the purified products to be human proinsulin and human insulin. Its radio-immune activity and receptor binding activity were almost the same as those of porcine insulin. Met-Lys-double-C peptide human proinsulin converted to human insulin with correct disulfide bonds. This strongly suggested the very flexible conformation of C-peptide. The addn. of Lysine between Met (initiator) and Phe (B1) made it easy to produce human insulin with N-terminal Phe (B1) from the human proinsulin analog in E. coli system.
ACCESSION NUMBER: 1999:575548 CAPLUS
DOCUMENT NUMBER: 131:296002
TITLE: Construction of Met-Lys-double-C peptide human proinsulin gene and its expression and characterization
AUTHOR(S): Chen, Yahui; Du, Yali; Tang, Jianguo
CORPORATE SOURCE: College of Life Sciences, Peking University, Beijing, 100871, Peop. Rep. China
SOURCE: Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao (1999), 15(4), 558-562
CODEN: ZSHXF2; ISSN: 1007-7626
PUBLISHER: Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao Bianweihui
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

L21 ANSWER 9 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB Latexin, a **carboxypeptidase** A inhibitor, is expressed in a cell type-specific manner in both central and peripheral nervous systems in the rat. In the neocortex, a specific subpopulation of neurons in layers V and VI expresses latexin. In the primary sensory ganglia, the expression is restricted to smaller diam. neurons. As a first step to clarify regulatory mechanisms underlying cell type-specific expression of latexin, we have detd. the organization of the rat latexin gene and analyzed its regulatory elements. The latexin gene spans approx. 5.8 kb, and consists of six exons and five introns. Three transcription initiation sites were mapped. The upstream region lacks typical TATA or CAAT boxes but has several GC-rich sites. To assess **promoter** activity, the luciferase reporter gene fused to the 5'-flanking region (6.4 kb) of the latexin gene was transiently transfected into several cell lines. Luciferase activity was 2-8 times higher in latexin-expressing cells (PC12) than non-expressing cells (NS20 and L6). Deletion anal. with PC12 cells revealed that a core **promoter** is located between

nucleotide positions -261 and -201 relative to the A of the initiation codon. Nerve growth factor (NGF)-responsive element(s) is located between positions -518 and -262, in which AP-1, AP-2 and NF-.kappa.B binding sites are found. Furthermore, we demonstrate that a 1.3 kb genomic fragment contg. the first intron has transcriptional enhancing activity in PC12 cells. These results suggest that up and downstream regulatory elements are involved in the control of cell type-specific expression of latexin.

ACCESSION NUMBER: 1999:340282 CAPLUS
DOCUMENT NUMBER: 131:154275
TITLE: Genomic organization and regulatory elements of the rat latexin gene, which is expressed in a cell type-specific manner in both central and peripheral nervous systems
AUTHOR(S): Miyasaka, Nobuhiko; Hatanaka, Yumiko; Jin, Ming-hao; Arimatsu, Yasuyoshi
CORPORATE SOURCE: Mitsubishi Kasei Institute of Life Sciences, Machida-shi, 194-8511, Japan
SOURCE: Mol. Brain Res. (1999), 69(1), 62-72
CODEN: MBREE4; ISSN: 0169-328X
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 40
REFERENCE(S):
(1) Amano, T; Proc Natl Acad Sci 1972, V69, P258 CAPLUS
(2) Arimatsu, Y; Development 1999, V126, P629 CAPLUS
(4) Arimatsu, Y; Neurosci Res 1994, V20, P131 CAPLUS
(5) Arimatsu, Y; Neuroscience 1999, V88, P93 CAPLUS
(6) Arimatsu, Y; Proc Natl Acad Sci 1992, V89, P8879 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 10 OF 170 CAPLUS COPYRIGHT 2001 ACS

AB Thrombin-activable fibrinolysis inhibitor (TAFI) is a recently described human plasma zymogen that is related to pancreatic **carboxypeptidase** B. The active form of TAFI (TAFIa), which is formed by thrombin cleavage of the zymogen, likely inhibits fibrinolysis by removal from partially degraded fibrin of the carboxyl-terminal lysine residues which act to stimulate plasminogen activation. The authors have isolated and characterized genomic clones which encompass the entire human TAFI gene from .lambda. phage and bacterial artificial chromosome genomic libraries. The complete TAFI gene contains 11 exons and spans approx. 48 kb of genomic DNA. The positions of intron/exon boundaries are conserved between the TAFI gene and the rat pancreatic **carboxypeptidase** A1, A2, and B and the human mast cell **carboxypeptidase** A genes, indicating that these carboxypeptidases arose from a common ancestral gene. However, the intron lengths diverge significantly among all of these genes. The TAFI **promoter** lacks a consensus TATA sequence, and transcription is initiated from multiple sites. Transient transfection of reporter plasmids contg. portions of the TAFI 5'-flanking region into mammalian cells allowed localization of the **promoter** and identified a .apprx.70 bp region crucial for liver-specific transcription. Sequence anal. of cDNA clones obtained from human liver RNA indicated that the TAFI transcript is polyadenylated at three different sites. The authors' findings will facilitate the assessment of the regulation of TAFI expression by transcriptional and/or posttranscriptional mechanisms. Furthermore, knowledge of the genomic structure of the TAFI gene will aid in the identification of mutations that may be assocd. with the tendency to either bleed or thrombose.

ACCESSION NUMBER: 1999:268720 CAPLUS
DOCUMENT NUMBER: 131:112173
TITLE: Characterization of the Gene Encoding Human TAFI

(Thrombin-Activable Fibrinolysis Inhibitor; Plasma Procarboxypeptidase B)
AUTHOR(S): Boffa, Michael B.; Reid, T. Scott; Joo, Emily; Nesheim, Michael E.; Koschinsky, Marlys L.
CORPORATE SOURCE: Departments of Biochemistry and Medicine, Queen's University, Kingston, ON, K7L 3N6, Can.
SOURCE: Biochemistry (1999), 38(20), 6547-6558
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 64
REFERENCE(S): (1) Anson, D; EMBO J 1984, V3, P1053 CAPLUS
(2) Azizkhan, J; Crit Rev Eukaryot Gene Expression 1993, V3, P229 CAPLUS
(3) Bajzar, L; Blood 1996, V88, P2093 CAPLUS
(4) Bajzar, L; J Biol Chem 1995, V270, P14477 CAPLUS
(5) Bajzar, L; J Biol Chem 1996, V271, P16603 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d l21 11-15 abs ibib

L21 ANSWER 11 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB **Carboxypeptidase** Y (CPY; EC 3.4.16.1) encoded by the PRC1 gene is a yeast vacuolar protease. It enters the vacuole as a zymogen, proCPY, which is activated by vacuolar enzymes, proteinase A (PrA) and proteinase B (PrB). We previously showed that active CPY was efficiently secreted from the Saccharomyces cerevisiae ssl1 (supersecretion of lysozyme) mutant carrying a multicopy plasmid which contains the PRC1 gene fused to an inducible GAL10 **promoter**. In this study, we detected PrA and PrB activities in the culture supernatant of the ssl1 mutant harboring the CPY expression plasmid. The N-terminal amino acid sequence of extracellular CPY coincided with that of the original vacuolar one. Furthermore, studies using protease inhibitors suggested that CPY was secreted into the medium in the form of a precursor and was mainly activated by extracellular PrB. The ssl1 mutant secreted CPY, PrA and PrB into the medium even with a single copy of the PRC1 gene. On the other hand, a cytoplasmic marker enzyme, glucose-6-phosphate dehydrogenase, and a vacuolar membrane-assocd. enzyme, .alpha.-mannosidase, were not detected in the medium, whether the PRC1 gene was overexpressed or not. It is suggested that secretion of vacuolar proteases is caused by characteristics of the ssl1 mutation or overexpression of the PRC1 gene.
ACCESSION NUMBER: 1999:115995 CAPLUS
DOCUMENT NUMBER: 130:264647
TITLE: Extracellular processing of carboxypeptidase Y secreted by a Saccharomyces cerevisiae ssl1 mutant strain
AUTHOR(S): Shiba, Yoichiro; Ichikawa, Kimihisa; Serizawa, Nobufusa; Yoshikawa, Hiroji
CORPORATE SOURCE: Biomedical Research Laboratories, Sankyo Co. Ltd., Fukushima, 971-8183, Japan
SOURCE: J. Ferment. Bioeng. (1998), 86(6), 545-549
CODEN: JFBIEX; ISSN: 0922-338X
PUBLISHER: Society for Fermentation and Bioengineering, Japan
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 39
REFERENCE(S): (1) Achstetter, T; Yeast 1985, V1, P139 CAPLUS

(2) Blachly-Dyson, E; J Cell Biol 1987, V104, P1183 CAPLUS
(3) Conibear, E; Cell 1995, V83, P513 CAPLUS
(4) Hasilik, A; Eur J Biochem 1978, V85, P599 CAPLUS
(5) Ichikawa, K; Biosci Biotech Biochem 1993, V57, P1686 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 12 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB Provided is an improved T7 promoter-driven protein expression system wherein basal expression in the absence of inducer is reduced to a level which permits the cloning and expression of toxic gene products while not influencing induced productivity. The invention also allows control of prodn. of heterologous proteins in an inducer concn.-dependent manner over a wide range of expression levels so that an optimum level of expression can be identified. The provided expression system comprises an operator sequence downstream of the T7 promoter sequence and a further operator sequence upstream of the T7 promoter sequence.

ACCESSION NUMBER: 1999:96377 CAPLUS
DOCUMENT NUMBER: 130:163973
TITLE: Novel T7 promoter-based expression system
INVENTOR(S): Pioli, David; Hockney, Robert Craig; Kara, Buhpendra Vallabh; Bundell, Kenneth Robert
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 56 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9905297	A1	19990204	WO 1998-GB2175	19980721
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9884533	A1	19990216	AU 1998-84533	19980721
EP 994954	A1	20000426	EP 1998-935181	19980721
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRIORITY APPLN. INFO.:			GB 1997-15660	19970725
			WO 1998-GB2175	19980721

REFERENCE COUNT: 3
REFERENCE(S): (1) Dubendorff, J; Journal of Molecular Biology 1991, V219(1), P45 CAPLUS
(2) ICI PLC; EP 0502637 A 1992, P2 CAPLUS
(3) Novagen; pET Expression System Information Package 1995

L21 ANSWER 13 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB A method of limiting prodrug activation to a specific cell type by targetting prodrug activating enzymes to that cell type as fusion proteins with cell-specific ligands is described. The cell-specific ligand may be an antibody, e.g. to a disease marker. Alternatively, the gene for the protein may be placed under control of a **promoter** that is only functional in the disease, e.g. a tumor marker gene. Chimeric genes for

fusion proteins of **carboxypeptidase** G2 (CPG2) and heavy and light chains of tibodies to carcinoembryonic a gen were constructed by std. methods. The fusion protein manufd. in animal cells dimerized through the dimerization domain of CPG2. The fusion protein was able to activate the prodrug PGP to the cytotoxic 4-[N,N-Bis(2-chloroethyl)amino]phenol. HCT116 cells transformed with the gene for this protein had an IC50 for PGP of 200 .mu.M compared to 1 .mu.M for the activated drug.

ACCESSION NUMBER: 1998:761969 CAPLUS
DOCUMENT NUMBER: 130:29189
TITLE: Fusion proteins of prodrug activating enzymes and targetting moieties and their therapeutic uses
INVENTOR(S): Emery, Stephen Charles; Blakey, David Charles
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 106 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9851787	A2	19981119	WO 1998-GB1294	19980505
WO 9851787	A3	19990401		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9872254	A1	19981208	AU 1998-72254	19980505
GB 2338484	A1	19991222	GB 1999-22815	19980505
EP 979292	A2	20000216	EP 1998-919380	19980505
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9808769	A	20000801	BR 1998-8769	19980505
ZA 9803931	A	19981110	ZA 1998-3931	19980508
NO 9905475	A	20000107	NO 1999-5475	19991109
PRIORITY APPLN. INFO.:			GB 1997-9421	19970510
			WO 1998-GB1294	19980505

L21 ANSWER 14 OF 170 CAPLUS COPYRIGHT 2001 ACS
AB In order to develop a prodn. process for **carboxypeptidase** Y (CPY, yeast vacuolar protease) secreted by Saccharomyces cerevisiae KS58-2D, medium compn., culture conditions, and expression systems were investigated. We found that the addn. of histidine to thiamin-free medium, in which CPY prodn. was almost negligible, raised the intracellular thiamin level, resulting in the increase of CPY prodn. On the basis of the choice of an expression system that uses an inducible GAL10 **promoter**, reassessment of histidine concn. in the medium, and optimization of the pH level during cultivation (pH 6.5), active CPY was secreted in a quantity of over 400 mg/l, which was more than tenfold that higher than that previously reported. The process developed could be easily scaled-up to industrial-scale fermn.

ACCESSION NUMBER: 1998:569432 CAPLUS
DOCUMENT NUMBER: 129:215747
TITLE: Process development for high-level secretory production of carboxypeptidase Y by Saccharomyces cerevisiae

AUTHOR(S): Shiba, Y.; Fukui, F.; Ichika[redacted] K.; Serizawa, N.; Yoshikawa, H.

CORPORATE SOURCE: Biomedical Research Laboratories, Sankyo Co. Ltd., Iwaki, 971-8183, Japan

SOURCE: Appl. Microbiol. Biotechnol. (1998), 50(1), 34-41
CODEN: AMBIDG; ISSN: 0175-7598

PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English

L21 ANSWER 15 OF 170 CAPLUS COPYRIGHT 2001 ACS

AB Saccharomyces cerevisiae was used as host for high-level prodn. of intact human parathyroid hormone (hPTH). The yield increased about 30-fold by changing from the constitutive MF.alpha. **promoter** to the inducible CUP1 **promoter** in the expression cassettes, use of another host strain, and optimization of growth conditions where esp. the pH value was crucial. The secreted products consisted mainly of intact hormone, hPTH(1-84). In addn., two C-terminally truncated forms that lacked the four or five last amino acid residues, hPTH(1-80) and hPTH(1-79), were identified. These hPTH forms migrated aberrantly by SDS-PAGE as 14-kDa proteins, while the real masses measured by mass spectrometry on HPLC-purified products were about 9kDa. Availability of such easily purified truncated forms will be valuable for studies of how the C-terminal residues affect the structure and function of the hormone. Combination of mutations and disruptions of the host genes encoding proteinase A, B, **carboxypeptidase** Y, and Kex1p or Mkc7p did not influence the C-terminal deletions. The secretion of hPTH could be enhanced by overexpression of the yeast syntaxin gene SSO2, but the total level of the hormone was not improved due to impaired growth. (c) 1998 Academic Press.

ACCESSION NUMBER: 1998:542186 CAPLUS
DOCUMENT NUMBER: 129:244155
TITLE: High-level production of human parathyroid hormone (hPTH) by induced expression in Saccharomyces cerevisiae
AUTHOR(S): Vad, Randi; Moe, Elin; Saga, Kirsti; Kvinnsland, Aina M. V.; Oyen, Tordis B.
CORPORATE SOURCE: Department of Biochemistry, University of Oslo, Oslo, N-0316, Norway
SOURCE: Protein Expression Purif. (1998), 13(3), 396-402
CODEN: PEXPEJ; ISSN: 1046-5928
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

=> d hist

(FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001

L1	1274	S	MALATE(W)SYNTHASE
L2	199155	S	PROMOTER
L3	203	S	GERMIN
L4	877	S	GLYOXYSOMAL
L5	0	S	ALEUTRONE(W)LAYER
L6	0	S	ALEUTRONE
L7	13735	S	CARBOXYPEPTIDASE
L8	8459	S	GLUTATHIONE(W)TRANSFERASE
L9	478	S	ALCA
L10	186	S	ALCR
L11	0	S	IACC(P)REPRESSOR
L12	13	S	IACC
L13	6132	S	434

```
L14         4174 S P2[redacted]
L15         3352 S TE[redacted]
L16        21064 S REPRESSOR
L17          459 S LAMBDA(W)BACTERIOPHAGE
L18           44 S L1(P)L2
L19           17 S L3(P)L2
L20           14 S L4(P)L2
L21          170 S L7(P)L2
L22           72 S L8(P)L2
L23           84 S L9(P)L2
L24           36 S L10(P)L2
L25            0 S L12(P)L2
L26          356 S L13(P)L16
L27          289 S L14(P)L16
L28          419 S L15(P)L16
L29           12 S L17(P)L16

=> d l22 1-10 abs ibib
```

L22 ANSWER 1 OF 72 CAPLUS COPYRIGHT 2001 ACS

AB The invention relates to the gene promoter region for the 27 kD subunit of the glutathione-S-transferase , isoenzyme II (GST-II-27), or a deleted fragment thereof which retains the activity of the gene promoter region. Such promoters are constitutive in tubers and can therefore be used to control the expression of a gene to prevent or inhibit sprouting of tubers. Preferably, the gene promoter is the maize GST-II-27.

ACCESSION NUMBER: 2000:227792 CAPLUS
DOCUMENT NUMBER: 132:261381
TITLE: Use of plant promoter GST-II-27 to prevent or inhibit sprouting of tubers in transgenic potato
INVENTOR(S): Robertson, Nicola Mary; Paine, Jacqueline Ann Mary; Jepson, Ian
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 53 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000018930	A1	20000406	WO 1999-GB3021	19990913
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9958733	A1	20000417	AU 1999-58733	19990913
PRIORITY APPLN. INFO.:			GB 1998-20970	19980925
			WO 1999-GB3021	19990913

REFERENCE COUNT: 11
REFERENCE(S): (1) Barry, G; WO 9428149 A 1994 CAPLUS
(2) Bevan, M; WO 9711189 A 1997 CAPLUS
(3) Caddick, M; WO 9321334 A 1993 CAPLUS
(4) Ebneth, M; WO 9906578 A 1999 CAPLUS
(5) Greenland, A; WO 9704116 A 1997 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 2 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB Nuclear factor (NF1) family proteins, which are encoded by four different genes (NF1-A, NF1-B, NF1-C and NF1-X), bind to the palindromic sequence and regulate the expression of many viral and cellular genes. We have previously purified NF1-A and NF1-B from rat liver as factors that bind to the silencer in the **glutathione transferase** P gene, and have also reported the repression domain of NF1-A. In the present study, we cloned five cDNA species (NF1-B1, NF1-B2, NF1-B3, NF1-C2 and NF1-X1) and compared their expression profiles and the affinity and specificity of the DNA binding of these NF1 family members. By Northern blot anal., we found that the expression profiles of the NF1s are indistinguishable in the various tissues of the rat. The DNA-binding affinities of NF1-A and NF1-X are higher than those of NF1-B and NF1-C, whereas all four NF1 proteins showed the same DNA-binding specificity. Transfection analyses revealed that the function of NF1-B on the transcriptional regulation differed between NF1-B isoforms and was affected by the factor(s) that bind to the **promoter** regions. In addn., we identified the transcriptional regulatory domain of NF1-B, which is enriched with proline and serine residues.

ACCESSION NUMBER: 1999:602789 CAPLUS
DOCUMENT NUMBER: 131:319222
TITLE: Expression, DNA-binding specificity and transcriptional regulation of nuclear factor 1 family proteins from rat
AUTHOR(S): Osada, Shigehiro; Matsubara, Tsukasa; Daimon, Shoko; Terazu, Yoshie; Xu, Mingxu; Nishihara, Tsutomu; Imagawa, Masayoshi
CORPORATE SOURCE: Laboratory of Environmental Biochemistry, Graduate School of Pharmaceutical Sciences, Osaka University, Suita, 565-0871, Japan
SOURCE: Biochem. J. (1999), 342(1), 189-198
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 43
REFERENCE(S): (1) Alevizopoulos, A; Genes Dev 1995, V9, P3051 CAPLUS
(2) Bernier, D; Mol Cell Biol 1993, V13, P1619 CAPLUS
(3) Bushmeyer, S; J Biol Chem 1995, V270, P30213 CAPLUS
(4) Chaudhry, A; Dev Dyn 1997, V208, P313 CAPLUS
(5) Chaudhry, A; J Biol Chem 1998, V273, P18538 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 3 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB The rat glutathione S-transferase-A3-subunit (GSTA3) gene is a member of the class Alpha GSTs, which the authors have previously reported to be overexpressed in anti-cancer-drug-resistant cells. In this study, the authors report the isolation and characterization of the entire rat GSTA3 (rGST Yc1) subunit gene. The rat GSTA3 subunit gene is approx. 15 kb in length and consists of seven exons interrupted by introns of different lengths. Exon 1, with a length of 219 bp, contains only the 5'-untranslated region of the gene. Each exon-intron splicing junction exhibited the consensus sequence for a mammalian splice site. The transcription start site and exon 1 of rat GSTA3 were characterized by a combination of primer extension and rapid amplification of the cDNA ends. Position +1 was identified 219 bp upstream of the first exon-intron splicing junction. The proximal promoter region of the rat GSTA3 subunit gene does not contain typical TATA or CAAT boxes. A computer-based search

for potential transcription-factor binding sites revealed the existence of a no. of motifs such as anti-oxidant-responsive element, ras-response element, activator protein-1, nuclear factor-.kappa.B, cAMP-response-element-binding protein, Barbie box and E box. The functional activity of the regulatory region of the rat GSTA3 subunit gene was shown by its ability to drive the expression of a chloramphenicol acetyltransferase reporter gene in rat mammary carcinoma cells, and its activity was greater in melphalan-resistant cells known to have transcriptional activation of this gene by previous studies. The structure of the gene, with a large intron upstream of the translation-initiation site, may explain why the isolation of this promoter has been so elusive. This information will provide the opportunity to examine the involvement of the rat GSTA3 subunit gene in drug resistance and carcinogenesis.

ACCESSION NUMBER: 1999:456834 CAPLUS
DOCUMENT NUMBER: 131:224234
TITLE: Genomic cloning and characterization of the rat glutathione S-transferase-A3-subunit gene
AUTHOR(S): Fotouhi-Ardakani, Nasser; Batist, Gerald
CORPORATE SOURCE: McGill Center for Translational Research in Cancer, Lady Davis Institute for Medical Research, Sir Mortimer B. Davis-Jewish General Hospital, Montreal, PQ, H3T 1E2, Can.
SOURCE: Biochem. J. (1999), 339(3), 685-693
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 50
REFERENCE(S):
(1) Altschul, S; Nucleic Acids Res 1997, V25, P3389 CAPLUS
(2) Ames, G; Cell 1986, V47, P323 CAPLUS
(3) Angel, P; Cell 1987, V49, P729 CAPLUS
(4) Anthoney, D; Cancer Res 1996, V56, P1374 CAPLUS
(5) Antonsson, C; J Biol Chem 1995, V270, P13968 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 4 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB The most well-documented biochem. property of p53 is its ability to transcriptionally activate genes. Many of the genes which are activated by p53 expression prior to the onset of apoptosis are predicted to encode proteins which could generate or respond to oxidative stress, including one that is implicated in apoptosis within plant meristems. P53 may result in apoptosis through a three-step process: (i) the transcriptional induction of specific redox-related genes; (ii) the formation of reactive oxygen species (ROS); and (iii) the oxidative degrdn. of mitochondrial components, rapidly leading to cell death. Transcription of other genes is decreased by p53. Examn. of the level of transcription of p53-induced or -repressed genes can be used to det. p53 status, to diagnose cancer, and to evaluate cytotoxicity or carcinogenicity of a test agent. Thus, colorectal cancer line DLD-1 was infected with replication-defective adenovirus encoding p53. SAGE tags were generated from mRNAs of the adenovirus-infected and control cells. Only 14 transcripts of 7,202 were expressed at levels >10-fold greater in p53-expressing than in control cells and only 20 transcripts were expressed at levels <10-fold lower in the p53-expressing cells. One of the p53-induced genes, PIG-3, was localized to chromosome 2p. The PIG-3 protein is "highly related" to TED2, a plant NADPH oxidoreductase. A p53-responsive element was defined in the PIG-3 gene **promoter**. PIG-1 belongs to the galectin family; PIG-4 encodes a serum amyloid protein that can be induced by oxidative stress; PIG-6 is a homolog of proline oxidoreductase; PIG-7 can be induced by TNF-.beta.; PIG-8 is the human homolog of mouse gene Ei24

whose expressio[redacted]is induced in a p53-dependent m[redacted]er by etoposide; and PIG-12 is a nov[redacted] member of the microsomal **gluta[redacted]one transferase** family of genes.

ACCESSION NUMBER: 1999:220080 CAPLUS
DOCUMENT NUMBER: 130:250709
TITLE: Cancer diagnosis using probes for p53-induced genes
INVENTOR(S): Vogelstein, Bert; Kinzler, Kenneth W.; Polyak, Kornelia
PATENT ASSIGNEE(S): The Johns Hopkins University, USA
SOURCE: PCT Int. Appl., 73 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9914356	A2	19990325	WO 1998-US19300	19980917
WO 9914356	A3	19990729		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9893173	A1	19990405	AU 1998-93173	19980917
EP 1015624	A2	20000705	EP 1998-946079	19980917
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRIORITY APPLN. INFO.:			US 1997-59153	19970917
			US 1998-79817	19980330
			WO 1998-US19300	19980917

L22 ANSWER 5 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB Glutathione-S-Transferases (GSTs) comprise a family of isoenzymes that provide protection to mammalian cells against electrophilic metabolites of carcinogens and reactive oxygen species. Previous studies have shown that the CpG-rich promoter region of the .pi.-class gene GSTP1 is methylated at single restriction sites in the majority of prostate cancers. To understand the nature of abnormal methylation of the GSTP1 gene in prostate cancer the authors undertook a detailed anal. of methylation at 131 CpG sites spanning the promoter and body of the gene. The results show that DNA methylation is not confined to specific CpG sites in the promoter region of the GSTP1 gene but is extensive throughout the CpG island in prostate cancer cells. Furthermore the authors found that both alleles are abnormally methylated in this region. In normal prostate tissue, the entire CpG island was unmethylated, but extensive methylation was found outside the island in the body of the gene. Loss of GSTP1 expression correlated with DNA methylation of the CpG island in both prostate cancer cell lines and cancer tissues whereas methylation outside the CpG island in normal prostate tissue appeared to have no effect on gene expression.

ACCESSION NUMBER: 1999:152738 CAPLUS
DOCUMENT NUMBER: 130:309899
TITLE: Detailed methylation analysis of the glutathione S-transferase .pi. (GSTP1) gene in prostate cancer
AUTHOR(S): Millar, Douglas S.; Ow, Kim K.; Paul, Cheryl L.; Russell, Pamela J.; Molloy, Peter L.; Clark, Susan J.

CORPORATE SOURCE: Kanemratsu Laboratories, Roy[redacted] Prince Alfred Hospital,
Canmperdown, 2050, Australia
SOURCE: Oncogene (1999), 18(6), 1313-1324
CODEN: ONCNES; ISSN: 0950-9232
PUBLISHER: Stockton Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 38
REFERENCE(S):
(1) Batist, G; J Biol Chem 1986, V261, P15544 CAPLUS
(2) Baylin, S; Advances in Cancer Research 1998, V72, P141 CAPLUS
(3) Clark, S; DNA and Nucleoprotein Structure In Vivo 1995, P123 CAPLUS
(4) Clark, S; Gene 1997, V195, P67 CAPLUS
(5) Clark, S; Laboratory Methods for the detection of mutations and polymorphisms in DNA 1997, P151 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 6 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB The sequence and exon-intron structure of the human class mu GSTM3 glutathione transferase gene and its orientation with respect to the remainder of the human class mu GSTM gene cluster were detd. The GSTM3 gene is 2847 bp long and is thus considerably shorter than the other class mu genes in the cluster, which range in size from 5325 to 7212 bp. Outside the protein-coding region, the GSTM3 gene does not share significant sequence similarity with other class mu glutathione transferase genes. Identification of overlapping cosmid clones that span the region between GSTM5, the next nearest glutathione transferase gene, and GSTM3 showed that the two genes are about 20,000 bp apart. PCR primers developed from sequences 3'-downstream from the GSTM5 gene were used to identify clones contg. the GSTM3 gene. Amplification with these primers showed that the orientation of the GSTM3 gene is 5'-GSTM5-3'-3'-GSTM3-5'. Long-range PCR reactions confirmed this orientation both in the GSTM-YAC2 YAC clone, which contains the five class mu glutathione transferase genes on chromosome 1, and in human DNA. This tail-to-tail orientation is consistent with an evolutionary model of class mu glutathione transferase divergence from a pair of tail-to-tail "M1-like" and "M3-like" class mu glutathione transferase genes that was present at the mammalian radiation to the current organization of multiple head-to-tail M1-like genes tail-to-tail with a single M3-like gene with distinct structural properties and expression patterns. (c) 1999 Academic Press.
ACCESSION NUMBER: 1999:37426 CAPLUS
DOCUMENT NUMBER: 130:262862
TITLE: Distinctive structure of the human GSTM3 gene-inverted orientation relative to the mu class glutathione transferase gene cluster
AUTHOR(S): Patskovsky, Yury V.; Huang, Ming-Qian; Takayama, Tetsuji; Listowsky, Irving; Pearson, William R.
CORPORATE SOURCE: Department of Biochemistry, Albert Einstein College of Medicine, Bronx, NY, 10461, USA
SOURCE: Arch. Biochem. Biophys. (1999), 361(1), 85-93
CODEN: ABBIA4; ISSN: 0003-9861
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

REFERENCE COUNT: 36
REFERENCE(S): (2) Bairoch, A; Nucleic Acids Res 1996, V24, P21 CAPLUS
(3) Batzer, M; J Mol Evol 1996, V42, P3 CAPLUS
(4) Board, P; Biochem J 1997, V328, P929 CAPLUS
(5) Campbell, E; J Biol Chem 1990, V265, P9188 CAPLUS
(6) Church, G; Proc Natl Acad Sci USA 1984, V81, P1991 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 7 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB We have isolated and characterized a human glutathione transferase A4 (hGSTA4) subunit gene from a yeast artificial chromosome contg. several other glutathione transferase alpha genes and pseudogenes. The homodimeric protein hGSTA4-4, is involved in the detoxification of 4-hydroxynonenal and other reactive electrophiles produced by oxidative metab., and may have a significant role in protecting intracellular components from oxidative damage. The hGSTA4 gene spans nearly 18 kb, contains seven exons, maps onto chromosome 6p12, and lies in close proximity to the 7SK small nuclear RNA gene in a head-to-tail orientation.
The intron/exon borders conform to the std. rules, an open reading frame is present beginning at position 154 in exon 2, and the stop codon is at position 822 in exon 7. The transcription initiation site has been detd. by primer extension anal. and is located 135 bp upstream of intron 1. Isolation and sequencing of the hGSTA4 gene 5'-flanking region revealed it to be devoid of TATA or CCAAT boxes but it does contain an initiator element overlapping the transcription start site, a GC box and putative binding sites for transcription factors AP1, STAT, GATA1 and NF-.kappa.B. Reverse transcription-PCR anal. revealed that hGSTA4 mRNA was present in all the tissues tested, although in low amts., suggesting that this subunit may be ubiquitously expressed.
ACCESSION NUMBER: 1999:11117 CAPLUS
DOCUMENT NUMBER: 130:192566
TITLE: Genomic organization, 5'-flanking region and chromosomal localization of the human glutathione transferase A4 gene
AUTHOR(S): Desmots, Fabienne; Rauch, Claudine; Henry, Catherine; Guillouzo, Andre; Morel, Fabrice
CORPORATE SOURCE: INSERM U456, Detoxication et Reparation Tissulaire, Faculte de Pharmacie, Rennes, 35043, Fr.
SOURCE: Biochem. J. (1998), 336(2), 437-442
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 34
REFERENCE(S): (1) Board, P; Biochem J 1997, V328, P929 CAPLUS
(2) Board, P; Biochem J 1998, V330, P827 CAPLUS
(3) Board, P; Proc Natl Acad Sci USA 1987, V84, P2377 CAPLUS
(4) Briggs, M; Science 1986, V234, P47 CAPLUS
(5) Driscoll, C; Nucleic Acids Res 1994, V22, P722 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 8 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB Promoter regions derived from the human glutathione S-transferase (GST) .alpha. gene cluster located on chromosome 6p12 were studied: the identical proximal promoters of the GST A1 and GST A2 genes and a proximal promoter of a pseudogene of this class. The sequence of the pseudogene promoter differs in four single nucleotides at positions -86, -66, -41,

and -13, and a [redacted]ncrit. TTT insertion at positi[redacted] -71 to -69 from the GST
A1/A2 promoter. Here, it was shown that the GST A1/A2 proximal promoters differed by a factor of 3.4 in their activity from the proximal pseudogene
promoter. Therefore, the functional significance of single base exchanges
was examd. by introducing individual point mutations at the four positions
within the proximal GST A1/A2 promoter. In functional tests in transiently transfected human hepatoblastoma HepG2 cells the base exchange
at position -13 showed no effect, whereas mutations at position -41 or -86
diminished the promoter activity to a level comparable to the pseudogene promoter. Promoter fragments of both genes spanning over these four sites
were analyzed in a heterologous promoter context for their functionality in HepG2 cells. Moreover, gel shift expts. showed specific binding of nuclear proteins to these promoter fragments. The results show that in the proximal GST A1/A2 promoter the sites at position -41 or -86 are essential for the binding of activating transcription factor complexes.
(c) 1998 Academic Press.

ACCESSION NUMBER: 1998:722335 CAPLUS
DOCUMENT NUMBER: 130:76999
TITLE: Identification of two activating elements in the proximal **promoter** region of the human **glutathione transferase**-A1 and -A2 genes
AUTHOR(S): Lorper, Michael; Clairmont, Annette; Carlberg, Carsten; Sies, Helmut
CORPORATE SOURCE: Institut fur Physiologische Chemie I and Biologisch-Medizinisches Forschungszentrum, Heinrich-Heine Universitit, Dusseldorf, D-40001, Germany
SOURCE: Arch. Biochem. Biophys. (1998), 359(1), 122-127
CODEN: ABBIA4; ISSN: 0003-9861
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 21
REFERENCE(S):
(1) Board, P; Biochem J 1997, V328, P929 CAPLUS
(3) Bradford, M; Anal Biochem 1976, V72, P248 CAPLUS
(4) Clairmont, A; Cancer Res 1994, V54, P1319 CAPLUS
(5) Eickelmann, P; Eur J Biochem 1995, V229, P21 CAPLUS
(6) Friling, R; Proc Natl Acad Sci USA 1992, V89, P668 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 9 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB Glutathione S-transferases (GSTs) are a family of isoenzymes that play an important role in protecting cells from cytotoxic and carcinogenic agents.
The .pi.-class GST has been assocd. with preneoplastic and neoplastic changes. Recently, it has been reported that regulatory sequences near the GSTP1 gene, which encodes the human .pi.-class GST, are commonly hypermethylated in prostatic carcinomas. In the present study, the authors studied more than 300 primary human tumors originating in other organs for aberrant methylation of GSTP1 using methylation-specific PCR. GSTP1 hypermethylation was most frequent in breast and renal carcinoma, showing aberrant methylation in 30 and 20% of the cases, resp. Other tumor types showed promoter methylation only rarely or not at all.
Hypermethylation of GSTP1 was assocd. with loss of expression demonstrated

by immunohistochem. The authors' results suggest that aberrant methylation of GSTP1 may contribute to the carcinogenetic process in breast and renal carcinomas.

ACCESSION NUMBER: 1998:671803 CAPLUS
DOCUMENT NUMBER: 130:50584
TITLE: Inactivation of glutathione S-transferase P1 gene by promoter hypermethylation in human neoplasia
AUTHOR(S): Esteller, Manel; Corn, Paul G.; Urena, Jesus M.; Gabrielson, Edward; Baylin, Stephen B.; Herman, James G.
CORPORATE SOURCE: Tumor Biology, The Johns Hopkins Oncology Center, Baltimore, MD, 21231, USA
SOURCE: Cancer Res. (1998), 58(20), 4515-4518
CODEN: CNREA8; ISSN: 0008-5472
PUBLISHER: American Association for Cancer Research
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 25
REFERENCE(S): (1) Ban, N; Cancer Res 1996, V56, P3577 CAPLUS
(3) Cavalieri, E; Proc Natl Acad Sci USA 1997, V94, P10937 CAPLUS
(4) Daniel, V; Crit Rev Biochem Mol Biol 1993, V28, P173 CAPLUS
(7) Harries, L; Carcinogenesis (Lond) 1997, V18, P641 CAPLUS
(8) Helzlsouer, K; J Natl Cancer Inst 1998, V90, P512 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 10 OF 72 CAPLUS COPYRIGHT 2001 ACS
AB Screening of a genomic mouse DNA library with a glutathione S-transferase class mu cDNA probe resulted in the identification of mGSTM5, a novel member of the murine glutathione S-transferase class mu gene family. Here we present the sequence of the promoter region, the exon-intron organization of the gene and the isolation and characterization of its complete cDNA. Conceptual translation of the cDNA sequence revealed that several amino acid positions have been changed in "invariant" mu class signature sequences in mGSTM5. Reverse transcriptase polymerase chain reaction using gene specific primers revealed that mGSTM5 is uniquely expressed in mouse liver, stomach and small intestine.

ACCESSION NUMBER: 1998:226422 CAPLUS
DOCUMENT NUMBER: 128:317840
TITLE: Identification of a novel murine glutathione S-transferase class mu gene
AUTHOR(S): De Bruin, Wieke C. C.; Te Morsche, Rene H. M.; Wagenmans, Muriel J. M.; Alferink, Jeroen C.; Townsend, Alan J.; Wieringa, Be; Peters, Wilbert H. M.
CORPORATE SOURCE: Department of Gastroenterology, St. Radboud University Hospital, Nijmegen, 6500 HB, Neth.
SOURCE: Biochem. J. (1998), 330(2), 623-626
CODEN: BIJOAK; ISSN: 0264-6021
PUBLISHER: Portland Press Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

=> d 123 1-10 abs ibib

L23 ANSWER 1 OF 84 CAPLUS COPYRIGHT 2001 ACS
AB An agriculturally acceptable hydrolyzable ester is used in the control of expression of a plant gene, said control being effected by an inducible